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(54) Title: VACCINE COMPOSITION

(57) Abstract: The present invention relates to an immuno-protective and non-toxic Gram-negative bleb vaccine suitable for paediatric use. Examples of the Gram-negative strains from which the blebs are made are *N. meningitidis*, *M. catarrhalis* and *H. influenzae*. The blebs of the invention are improved by one or more genetic changes to the chromosome of the bacterium, including up-regulation of protective antigens, down-regulation of immunodominant non-protective antigens, and detoxification of the Lipid A moiety of LPS.

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## VACCINE COMPOSITION

### FIELD OF THE INVENTION

The present invention relates to the field of Gram-negative bacterial vaccine  
5 compositions, their manufacture, and the use of such compositions in medicine. More particularly it relates to the field of novel outer-membrane vesicle (or bleb) vaccines, and advantageous methods of rendering these vaccines more effective and safer.

### BACKGROUND OF THE INVENTION

10 Gram-negative bacteria are separated from the external medium by two successive layers of membrane structures. These structures, referred to as the cytoplasmic membrane and the outer membrane (OM), differ both structurally and functionally. The outer membrane plays an important role in the interaction of pathogenic bacteria with their respective hosts. Consequently, the surface exposed  
15 bacterial molecules represent important targets for the host immune response, making outer-membrane components attractive candidates in providing vaccine, diagnostic and therapeutics reagents.

Whole cell bacterial vaccines (killed or attenuated) have the advantage of supplying multiple antigens in their natural micro-environment. Drawbacks around  
20 this approach are the side effects induced by bacterial components such as endotoxin and peptidoglycan fragments. On the other hand, acellular subunit vaccines containing purified components from the outer membrane may supply only limited protection and may not present the antigens properly to the immune system of the host.

Proteins, phospholipids and lipopolysaccharides are the three major  
25 constituents found in the outer-membrane of all Gram-negative bacteria. These molecules are distributed asymmetrically: membrane phospholipids (mostly in the inner leaflet), lipooligosaccharides (exclusively in the outer leaflet) and proteins (inner and outer leaflet lipoproteins, integral or polytopic membrane proteins). For many bacterial pathogens which impact on human health, lipopolysaccharide and outer-  
30 membrane proteins have been shown to be immunogenic and amenable to confer protection against the corresponding disease by way of immunization.

The OM of Gram-negative bacteria is dynamic and, depending on the environmental conditions, can undergo drastic morphological transformations. Among these manifestations, the formation of outer-membrane vesicles or “blebs” has been studied and documented in many Gram-negative bacteria (Zhou, L *et al.* 1998. *FEMS Microbiol. Lett.* 163: 223-228). Among these, a non-exhaustive list of bacterial pathogens reported to produce blebs include: *Bordetella pertussis*, *Borrelia burgdorferi*, *Brucella melitensis*, *Brucella ovis*, *Chlamydia psittaci*, *Chlamydia trachomatis*, *Escherichia coli*, *Haemophilus influenzae*, *Legionella pneumophila*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pseudomonas aeruginosa* and *Yersinia enterocolitica*. Although the biochemical mechanism responsible for the production of OM blebs is not fully understood, these outer membrane vesicles have been extensively studied as they represent a powerful methodology in order to isolate outer-membrane protein preparations in their native conformation. In that context, the use of outer-membrane preparations is of particular interest to develop vaccines against *Neisseria*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Pseudomonas aeruginosa* and *Chlamydia*. Moreover, outer membrane blebs combine multiple proteinaceous and non-proteinaceous antigens that are likely to confer extended protection against intra-species variants.

In comparison with the other, more widely used, types of bacterial vaccine (whole cell bacterial and purified subunit vaccines), the inventors will show that outer membrane bleb vaccines (if modified in certain ways) may represent the ideal compromise.

The wide-spread use of bacterial subunit vaccines has been due to the intensive study of bacterial surface proteins that have been found to be useful in vaccine applications [for instance *B. pertussis* pertactin]. These proteins are loosely associated with the bacterial outer membrane and can be purified from culture supernatant or easily extracted from the bacterial cells. However it has also been shown that structural, integral outer membrane proteins are also protective antigens. Examples are PorA for *N. meningitidis* serogroup B; D15 for *H. influenzae*; OMP CD for *M. catarrhalis*; OMP F for *P. Aeruginosa*. Such proteins however have rather specific structural features, particularly multiple amphipathic  $\beta$ -sheets, which complicates their straightforward use as purified (recombinant) subunit vaccines.

In addition, it has become clear that multiple component vaccines are needed (in terms of bacterial surface proteins and integral membrane proteins) to supply a reasonable level of protection. For instance, in the case of *B. pertussis* subunit vaccines multicomponent vaccines are superior to mono or bicomponent products.

5 In order to incorporate integral outer-membrane proteins into such a subunit product, native (or near-native) conformational folding of the proteins must be present in the product in order to have a useful immunological effect. The use of excreted outer membrane vesicles or blebs may be an elegant solution to the problem of including protective integral membrane proteins into a subunit vaccine whilst still  
10 ensuring that they fold properly.

*N. meningitidis* serogroup B (menB) excretes outer membrane blebs in sufficient quantities to allow their manufacture on an industrial scale. Such multicomponent outer-membrane protein vaccines from naturally-occurring menB strains have been found to be efficacious in protecting teenagers from menB disease  
15 and have become registered in Latin America. An alternative method of preparing outer-membrane vesicles is via the process of detergent extraction of the bacterial cells (EP 11243).

Examples of bacterial species from which bleb vaccines can be made are the following.

20

*Neisseria meningitidis*:

*Neisseria meningitidis* (meningococcus) is a Gram-negative bacterium frequently isolated from the human upper respiratory tract. It occasionally causes invasive bacterial diseases such as bacteremia and meningitis. The incidence of  
25 meningococcal disease shows geographical seasonal and annual differences (Schwartz, B., Moore, P.S., Broome, C.V.; Clin. Microbiol. Rev. 2 (Supplement), S18-S24, 1989). Most disease in temperate countries is due to strains of serogroup B and varies in incidence from 1-10/100,000/year total population sometimes reaching higher values (Kaczmarek, E.B. (1997), Commun. Dis. Rep. Rev. 7: R55-9, 1995;  
30 Scholten, R.J.P.M., Bijlmer, H.A., Poolman, J.T. et al. Clin. Infect. Dis. 16: 237-246, 1993; Cruz, C., Pavez, G., Aguilar, E., et al. Epidemiol. Infect. 105: 119-126, 1990).



Age-specific incidences in the two high risk-groups, infants and teenagers, reach higher levels.

Epidemics dominated by serogroup A meningococci occur, mostly in central Africa, sometimes reaching levels up to 1000/100,000/year (Schwartz, B., Moore, P.S., Broome, C.V. Clin. Microbiol. Rev. 2 (Supplement), S18-S24, 1989). Nearly all cases of meningococcal disease as a whole are caused by serogroup A, B, C, W-135 and Y meningococci. A tetravalent A, C, W-135, Y capsular polysaccharide vaccine is available (Armand, J., Arminjon, F., Mynard, M.C., Lafaix, C., J. Biol. Stand. 10: 335-339, 1982).

The polysaccharide vaccines are currently being improved by way of chemically conjugating them to carrier proteins (Lieberman, J.M., Chiu, S.S., Wong, V.K., et al. JAMA 275 : 1499-1503, 1996). A serogroup B vaccine is not available, since the B capsular polysaccharide is non-immunogenic, most likely because it shares structural similarity to host components (Wyle, F.A., Artenstein, M.S., Brandt, M.L. et al. J. Infect. Dis. 126: 514-522, 1972; Finne, J.M., Leinonen, M., Mäkelä, P.M. Lancet ii.: 355-357, 1983).

For many years efforts have been focused on developing meningococcal outer membrane based vaccines (de Moraes, J.C., Perkins, B., Camargo, M.C. et al. Lancet 340: 1074-1078, 1992; Bjune, G., Hoiby, E.A. Gronnesby, J.K. et al. 338: 1093-1096, 1991). Such vaccines have demonstrated efficacies from 57% - 85% in older children (>4 years) and adolescents. Most of these efficacy trials were performed with OMV (outer membrane vesicles, derived by LPS depletion from blebs) vaccines derived from wild-type *N. meningitidis* B strains.

Many bacterial outer membrane components are present in these vaccines, such as PorA, PorB, Rmp, Opc, Opa, FrpB and the contribution of these components to the observed protection still needs further definition. Other bacterial outer membrane components have been defined (using animal or human antibodies) as potentially being relevant to the induction of protective immunity, such as TbpB, NspA (Martin, D., Cadieux, N., Hamel, J., Brodeux, B.R., J. Exp. Med. 185: 1173-1183, 1997; Lissolo, L., Maître-Wilmotte, C., Dumas, p. et al., Inf. Immun. 63: 884-890, 1995). The mechanism of protective immunity will involve antibody mediated bactericidal activity and opsonophagocytosis.

The frequency of *Neisseria meningitidis* infections has risen dramatically in the past few decades. This has been attributed to the emergence of multiple antibiotic resistant strains, and increased exposure due to an increase in social activities (for instance swimming pools or theatres). It is no longer uncommon to isolate *Neisseria*  
5 *meningitidis* strains that are resistant to some or all of the standard antibiotics. This phenomenon has created an unmet medical need and demand for new anti-microbial agents, vaccines, drug screening methods, and diagnostic tests for this organism.

*Moraxella catarrhalis*

10 *Moraxella catarrhalis* (also named *Branhamella catarrhalis*) is a Gram-negative bacterium frequently isolated from the human upper respiratory tract. It is responsible for several pathologies, the main ones being otitis media in infants and children, and pneumonia the elderly. It is also responsible for sinusitis, nosocomial infections and, less frequently, for invasive diseases.

15 Bactericidal antibodies have been identified in most adults tested (Chapman, AJ et al. (1985) J. Infect.Dis. 151:878). Strains of *M. catarrhalis* present variations in their capacity to resist serum bactericidal activity: in general, isolates from diseased individuals are more resistant than those who are simply colonized (Hol, C et al. (1993) Lancet 341:1281, Jordan, KL et al. (1990) Am.J.Med. 88 (suppl. 5A):28S). Serum resistance  
20 could therefore be considered as a virulence factor of the bacteria. An opsonizing activity has been observed in the sera of children recovering from otitis media.

The antigens targetted by these different immune responses in humans have not been identified, with the exception of OMP B1, a 84 kDa protein, the expression of which is regulated by iron, and that is recognized by the sera of patients with pneumonia (Sethi,  
25 S, et al. (1995) Infect.Immun. 63:1516), and of UspA1 and UspA2 (Chen D. et al.(1999), Infect.Immun. 67:1310).

A few other membrane proteins present on the surface of *M. catarrhalis* have been characterized using biochemical methods for their potential implication in the induction of a protective immunity (for review, see Murphy, TF (1996) Microbiol.Rev. 60:267). In a  
30 mouse pneumonia model, the presence of antibodies raised against some of them (UspA, CopB) favors a faster clearance of the pulmonary infection. Another polypeptide (OMP CD) is highly conserved among *M. catarrhalis* strains, and presents homologies with a

porin of *Pseudomonas aeruginosa*, which has been demonstrated to be efficacious against this bacterium in animal models.

*M. catarrhalis* produces outer membrane vesicles (Blebs). These Blebs have been isolated or extracted by using different methods (Murphy T.F., Loeb M.R. 1989. Microb. Pathog. 6: 159-174; Unhanand M., Maciver, I., Ramillo O., Arencibia-Mireles O., Argyle J.C., McCracken G.H. Jr., Hansen E.J. 1992. J. Infect. Dis. 165:644-650). The protective capacity of such Bleb preparations has been tested in a murine model for pulmonary clearance of *M. catarrhalis*. It has been shown that active immunization with Bleb vaccine or passive transfer of anti-Blebs antibody induces significant protection in this model (Maciver I., Unhanand M., McCracken G.H. Jr., Hansen, E.J. 1993. J. Infect. Dis. 168: 469-472).

### *Haemophilus influenzae*

*Haemophilus influenzae* is a non-motile Gram-negative bacterium. Man is its only natural host. *H. influenzae* isolates are usually classified according to their polysaccharide capsule. Six different capsular types designated 'a' through 'f' have been identified. Isolates that fail to agglutinate with antisera raised against one of these six serotypes are classified as nontypeable, and do not express a capsule.

*H. influenzae* type b (Hib) is clearly different from the other types in that it is a major cause of bacterial meningitis and systemic diseases. Nontypeable strains of *H. influenzae* (NTHi) are only occasionally isolated from the blood of patients with systemic disease. NTHi is a common cause of pneumonia, exacerbation of chronic bronchitis, sinusitis and otitis media. NTHi strains demonstrate a large variability as identified by clonal analysis, whilst Hib strains as a whole are more homogeneous.

Various proteins of *H. influenzae* have been shown to be involved in pathogenesis or have been shown to confer protection upon vaccination in animal models.

Adherence of NTHi to human nasopharyngeal epithelial cells has been reported (Read RC. et al. 1991. J. Infect. Dis. 163:549). Apart from fimbriae and pili (Brinton CC. et al. 1989. Pediatr. Infect. Dis. J. 8:S54; Kar S. et al. 1990. Infect. Immun. 58:903; Gildorf JR. et al. 1992. Infect. Immun. 60:374; St. Geme JW et al. 1991. Infect. Immun. 59:3366; St. Geme JW et al. 1993. Infect. Immun. 61: 2233), many adhesins have been

identified in NTHi. Among them, two surface exposed high-molecular-weight proteins designated HMW1 and HMW2 have been shown to mediate adhesion of NTHi to epithelial cells (St. Geme JW. et al. 1993. Proc. Natl. Acad. Sci. USA 90:2875). Another family of high-molecular-weight proteins has been identified in NTHi strains that lack  
5 proteins belonging to HMW1/HMW2 family. The NTHi 115-kDa Hia protein (Barenkamp SJ., St Geme S.W. 1996. Mol. Microbiol. In press) is highly similar to the Hsf adhesin expressed by *H. influenzae* type b strains (St. Geme JW. et al. 1996. J. Bact. 178:6281). Another protein, the Hap protein shows similarity to IgA1 serine proteases and has been shown to be involved in both adhesion and cell entry (St. Geme JW. et al. 1994.  
10 Mol. Microbiol. 14:217).

Five major outer membrane proteins (OMP) have been identified and numerically numbered. Original studies using *H. influenzae* type b strains showed that antibodies specific for P1 and P2 OMPs protected infant rats from subsequent challenge (Loeb MR. et al. 1987. Infect. Immun. 55:2612; Musson RS. Jr. et al.  
15 1983. J. Clin. Invest. 72:677). P2 was found to be able to induce bactericidal and opsonic antibodies, which are directed against the variable regions present within surface exposed loop structures of this integral OMP (Haase EM. et al. 1994 Infect. Immun. 62:3712; Troelstra A. et al. 1994 Infect. Immun. 62:779). The lipoprotein P4 also may induce bactericidal antibodies (Green BA. et al. 1991.  
20 Infect. Immun. 59:3191).

OMP P6 is a conserved peptidoglycan associated lipoprotein making up 1-5 % of the outer membrane (Nelson MB. et al. 1991. Infect. Immun. 59:2658). Later a lipoprotein of about the same molecular weight was recognized called PCP (P6 cross-reactive protein) (Deich RM. et al. 1990. Infect. Immun. 58:3388). A mixture of the  
25 conserved lipoproteins P4, P6 and PCP did not reveal protection as measured in a chinchilla otitis-media model (Green BA. et al. 1993. Infect. immun. 61:1950). P6 alone appears to induce protection in the chinchilla model (Demaria TF. et al. 1996. Infect. Immun. 64:5187).

A fimbrin protein (Miyamoto N., Bakaletz, LO. 1996. Microb. Pathog. 21:343)  
30 has also been described with homology to OMP P5, which itself has sequence homology to the integral *Escherichia coli* OmpA (Miyamoto N., Bakaletz, LO. 1996. Microb.

Pathog. 21:343; Munson RS. Jr. et al. 1993. Infect. Immun. 61:1017). NTHi seem to adhere to mucus by way of fimbriae.

In line with the observations made with gonococci and meningococci, NTHi expresses a dual human transferrin receptor composed of TbpA and TbpB when grown  
5 under iron limitation. Anti-TbpB antibody protected infant rats (Loosmore SM. et al. 1996. Mol. Microbiol. 19:575). Hemoglobin / haptoglobin receptor also have been described for NTHi (Maciver I. et al. 1996. Infect. Immun. 64:3703). A receptor for Haem:Hemopexin has also been identified (Cope LD. et al. 1994. Mol. Microbiol. 13:868). A lactoferrin receptor is also present amongst NTHi, but is not yet  
10 characterized (Schryvers AB. et al. 1989. J. Med. Microbiol. 29:121). A protein similar to neisserial FrpB-protein has not been described amongst NTHi.

An 80kDa OMP, the D15 surface antigen, provides protection against NTHi in a mouse challenge model. (Flack FS. et al. 1995. Gene 156:97). A 42kDa outer membrane lipoprotein, LPD is conserved amongst *Haemophilus influenzae* and  
15 induces bactericidal antibodies (Akkoyunlu M. et al. 1996. Infect. Immun. 64:4586). A minor 98kDa OMP (Kimura A. et al. 1985. Infect. Immun. 47:253), was found to be a protective antigen, this OMP may very well be one of the Fe-limitation inducible OMPs or high molecular weight adhesins that have been characterized thereafter. *H. Influenzae* produces IgA1-protease activity (Mulks MH., Shoberg RJ. 1994. Meth.  
20 Enzymol. 235:543). IgA1-proteases of NTHi have a high degree of antigenic variability (Lomholt H., van Alphen L., Kilian, M. 1993. Infect. Immun. 61:4575).

Another OMP of NTHi, OMP26, a 26-kDa protein has been shown to enhance pulmonary clearance in a rat model (Kyd, J.M., Cripps, A.W. 1998. Infect. Immun. 66:2272). The NTHi HtrA protein has also been shown to be a protective antigen.  
25 Indeed, this protein protected Chinchilla against otitis media and protected infant rats against *H. influenzae* type b bacteremia (Loosmore S.M. et al. 1998. Infect. Immun. 66:899).

Outer membrane vesicles (or blebs) have been isolated from *H. influenzae* (Loeb M.R., Zachary A.L., Smith D.H. 1981. J. Bacteriol. 145:569-604; Stull T.L.,  
30 Mack K., Haas J.E., Smit J., Smith A.L. 1985. Anal. Biochem. 150: 471-480). The vesicles have been associated with the induction of blood-brain barrier permeability (Wiwpelwey B., Hansen E.J., Scheld W.M. 1989 Infect. Immun. 57: 2559-2560), the

induction of meningeal inflammation (Mustafa M.M., Ramilo O., Syrogiannopoulos G.A., Olsen K.D., McCracken G.H. Jr., Hansen, E.J. 1989. J. Infect. Dis. 159: 917-922) and to DNA uptake (Concino M.F., Goodgal S.H. 1982 J. Bacteriol. 152: 441-450). These vesicles are able to bind and be absorbed by the nasal mucosal epithelium  
5 (Harada T., Shimuzu T., Nishimoto K., Sakakura Y. 1989. Acta Otorhinolarygol. 246: 218-221) showing that adhesins and/or colonization factors could be present in Blebs. Immune response to proteins present in outer membrane vesicles has been observed in patients with various *H. influenzae* diseases (Sakakura Y., Harada T., Hamaguchi Y., Jin C.S. 1988. Acta Otorhinolarygol. Suppl. (Stockh.) 454: 222-226; Harada T.,  
10 Sakakura Y., Miyoshi Y. 1986. Rhinology 24: 61-66).

*Pseudomonas aeruginosa*:

The genus *Pseudomonas* consists of Gram-negative, polarly flagellated, straight and slightly curved rods that grow aerobically and do not forms spores.  
15 Because of their limited metabolic requirements, *Pseudomonas spp.* are ubiquitous and are widely distributed in the soil, the air, sewage water and in plants. Numerous species of *Pseudomonas* such as *P. aeruginosa*, *P. pseudomallei*, *P. mallei*, *P. maltophilia* and *P. cepacia* have also been shown to be pathogenic for humans. Among this list, *P. aeruginosa* is considered as an important human pathogen since it  
20 is associated with opportunistic infection of immuno-compromised host and is responsible for high morbidity in hospitalized patients. Nosocomial infection with *P. aeruginosa* afflicts primarily patients submitted for prolonged treatment and receiving immuno-suppressive agents, corticosteroids, antimetabolites antibiotics or radiation.

The *Pseudomonas*, and particularly *P. aeruginosa*, produces a variety of toxins  
25 (such as hemolysins, fibrinolysins, esterases, coagulases, phospholipases, endo- and exo-toxins) that contribute to the pathogenicity of these bacteria. Moreover, these organisms have high intrinsic resistance to antibiotics due to the presence of multiple drug efflux pumps. This latter characteristic often complicates the outcome of the disease.

30 Due to the uncontrolled use of antibacterial chemotherapeutics the frequency of nosocomial infection caused by *P. aeruginosa* has increased considerably over the last 30 years. In the US, for example, the economic burden of *P. aeruginosa*

nosocomial infection is estimated to 4.5 billion US\$ annually. Therefore, the development of a vaccine for active or passive immunization against *P. aeruginosa* is actively needed (for review see Stanislavsky et al. 1997. FEMS Microbiol. Lett. 21: 243-277).

5 Various cell-associated and secreted antigens of *P. aeruginosa* have been the subject of vaccine development. Among *Pseudomonas* antigens, the mucoid substance, which is an extracellular slime consisting predominantly of alginate, was found to be heterogenous in terms of size and immunogenicity. High molecular mass  
10 alginate components (30-300 kDa) appear to contain conserved epitopes while lower molecular mass alginate components (10-30 kDa) possess conserved epitopes in addition to unique epitopes. Among surface-associated proteins, PcrV, which is part of the type III secretion-translocation apparatus, has also been shown to be an interesting target for vaccination (Sawa et al. 1999. Nature Medicine 5:392-398).

Surface-exposed antigens including O-antigens (O-specific polysaccharide of  
15 LPS) or H-antigens (flagellar antigens) have been used for serotyping due to their highly immunogenic nature. Chemical structures of repeating units of O-specific polysaccharides have been elucidated and these data allowed the identification of 31 chemotypes of *P. aeruginosa*. Conserved epitopes among all serotypes of *P. aeruginosa* are located in the core oligosaccharide and the lipid A region of LPS and  
20 immunogens containing these epitopes induce cross-protective immunity in mice against different *P. aeruginosa* immunotypes. The outer core of LPS was implicated to be a ligand for binding of *P. aeruginosa* to airway and ocular epithelial cells of animals. However, heterogeneity exists in this outer core region among different serotypes. Epitopes in the inner core are highly conserved and have been  
25 demonstrated to be surface-accessible, and not masked by O-specific polysaccharide.

To examine the protective properties of OM proteins, a vaccine containing *P. aeruginosa* OM proteins of molecular masses ranging from 20 to 100 kDa has been used in pre-clinical and clinical trials. This vaccine was efficacious in animal models against *P. aeruginosa* challenge and induced high levels of specific antibodies in  
30 human volunteers. Plasma from human volunteers containing anti-*P. aeruginosa* antibodies provided passive protection and helped the recovery of 87% of patients with severe forms of *P. aeruginosa* infection. More recently, a hybrid protein

containing parts of the outer membrane proteins OprF (amino acids 190-342) and OprI (amino acids 21-83) from *Pseudomonas aeruginosa* fused to the glutathione-S-transferase was shown to protect mice against a 975-fold 50% lethal dose of *P. aeruginosa* (Knapp et al. 1999. Vaccine. 17:1663-1669).

5

The present inventors have realised a number of drawbacks associated with the above wild-type bleb vaccines (either naturally occurring or chemically made).

Examples of such problems are the following:

- 10 - the presence of immunodominant but variable proteins on the bleb (PorA; TbpB, Opa [*N. meningitidis* B]; P2, P5 [non-typeable *H. influenzae*]) – such blebs being effective only against a restricted selection of bacterial species. Type-specificity of the bactericidal antibody response may preclude the use of such vaccines in infancy.
- 15 - the presence of unprotective (non relevant) antigens (Rmp, H8, ...) on the bleb – antigens that are decoys for the immune system
- the lack of presence of important molecules which are produced conditionally (for instance iron-regulated outer membrane proteins, IROMP's, in vivo regulated expression mechanisms) – such conditions are hard to control in bleb production in order to optimise the amount of antigen on the surface
- 20 - the low level of expression of protective, (particularly conserved) antigens (NspA, P6)
- the toxicity of the LPS remaining on the surface of the bleb
- 25 - the potential induction of an autoimmune response because of host-identical structures (for example the capsular polysaccharide in *Neisseria meningitidis* serogroup B, the lacto-N-neotetraose in *Neisseria* LPS, saccharide structure within ntHi LPS, saccharide structures within Pili).

Such problems may prevent the use of bleb vaccines as human vaccine reagents. This is particularly so for paediatric use (<4 years) where reactogenicity against bleb vaccines is particularly important, and where bleb vaccines (for instance the previously mentioned marketed MenB bleb vaccine) have been shown to be



ineffective at immuno-protecting. Accordingly, the present invention provides methods of alleviating the above problems using genetically engineered bacterial strains, which result in improved bleb vaccines. Such methods will be especially useful in the generation of new vaccines against bacterial pathogens such as *Neisseria meningitidis*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Pseudomonas aeruginosa*, and others.

The bleb vaccines of the invention are designed to focus the immune response on a few protective (preferably conserved) antigens or epitopes - formulated in a multiple component vaccine. Where such antigens are integral OMPs, the outer membrane vesicles of bleb vaccines will ensure their proper folding. This invention provides methods to optimize the OMP and LPS composition of OMV (bleb) vaccines by deleting immunodominant variable as well as non protective OMPs, by creating conserved OMPs by deletion of variable regions, by upregulating expression of protective OMPs, and by eliminating control mechanisms for expression (such as iron restriction) of protective OMPs. In addition the invention provides for the reduction in toxicity of lipid A by modification of the lipid portion or by changing the phosphoryl composition whilst retaining its adjuvant activity or by masking it. Each of these new methods of improvement individually improve the bleb vaccine, however a combination of one or more of these methods work in conjunction so as to produce an optimised engineered bleb vaccine which is immuno-protective and non-toxic - particularly suitable for paediatric use.

## SUMMARY OF THE INVENTION

The present invention provides a genetically-engineered bleb preparation from a Gram-negative bacterial strain characterized in that said preparation is obtainable by employing one or more processes selected from the following group:

- a) a process of reducing immunodominant variable or non-protective antigens within the bleb preparation comprising the steps of determining the identity of such antigen, engineering a bacterial strain to produce less or none of said antigen, and making blebs from said strain;
- b) a process of upregulating expression of protective, endogenous (and preferably conserved) OMP antigens within the bleb preparation

- comprising the steps of identifying such antigen, engineering a bacterial strain so as to introduce a stronger promoter sequence upstream of a gene encoding said antigen such that said gene is expressed at a level higher than in the non-modified bleb, and making blebs from said strain;
- 5 c) a process of upregulating expression of conditionally-expressed, protective (and preferably conserved) OMP antigens within the bleb preparation comprising the steps of identifying such an antigen, engineering a bacterial strain so as to remove the repressive control mechanisms of its expression (such as iron restriction), and making blebs from said strain;
- 10 d) a process of modifying lipid A portion of bacterial LPS within the bleb preparation, comprising the steps of identifying a gene involved in rendering the lipid A portion of LPS toxic, engineering a bacterial strain so as to reduce or switch off expression of said gene, and making blebs from said strain;
- 15 e) a process of modifying lipid A portion of bacterial LPS within the bleb preparation, comprising the steps of identifying a gene involved in rendering the lipid A portion of LPS less toxic, engineering a bacterial strain so as to introduce a stronger promoter sequence upstream of said gene such that said gene is expressed at a level higher than in the non-
- 20 modified bleb, and making blebs from said strain;
- f) a process of reducing lipid A toxicity within the bleb preparation and increasing the levels of protective antigens, comprising the steps of engineering the chromosome of a bacterial strain to incorporate a gene encoding a Polymyxin A peptide, or a derivative or analogue thereof, fused
- 25 to a protective antigen, and making blebs from said strain;
- g) a process of creating conserved OMP antigens on the bleb preparation comprising the steps of identifying such antigen, engineering a bacterial strain so as to delete variable regions of a gene encoding said antigen, and making blebs from said strain;
- 30 h) a process of reducing expression within the bleb preparation of an antigen which shares a structural similarity with a human structure and may be capable of inducing an auto-immune response in humans (such as the

capsular polysaccharide of *N. meningitidis* B), comprising the steps of identifying a gene involved in the biosynthesis of the antigen, engineering a bacterial strain so as to reduce or switch off expression of said gene, and making blebs from said strain; or

- 5 i) a process of upregulating expression of protective, endogenous (and preferably conserved) OMP antigens within the bleb preparation comprising the steps of identifying such antigen, engineering a bacterial strain so as to introduce into the chromosome one or more further copies of a gene encoding said antigen controlled by a heterologous, stronger  
10 promoter sequence, and making blebs from said strain.

Further aspects of the invention include, preferential processes for obtaining the above bleb preparation, including optimal positioning of strong promoters for the upregulation of expression of antigens within blebs, preferential antigens for  
15 upregulation and downregulation for various bacterial strains in order to obtain bleb preparations particularly suitable for vaccine use. Preferential formulations comprising the blebs of the invention are also provided which are particularly suitable for global vaccines against certain disease states. Vectors for producing the blebs of the invention, and modified bacterial strains from which the blebs of the invention are  
20 produced are still further aspects of the invention.

The present invention provides for the first time a bleb vaccine which is immuno-protective and non-toxic when used with children under 4 years of age.

## **BRIEF DESCRIPTION OF THE DRAWINGS**

25

**Figure 1:** Reactivity of the 735 mAb on different colonies.

**Figure 2:** Reactivities of specific monoclonal antibodies by whole cell Elisa.

30 **Figure 3:** Schematic representation of the pCMK vectors used to deliver genes, operons and/or expression cassettes in the genome of *Neisseria meningitidis*.

**Figure 4:** Analysis of PorA expression in total protein extracts of recombinant *N. meningitidis* serogroupB (H44/76 derivatives). Total proteins were recovered from *cps*- (lanes 3 and 4), *cps- porA::pCMK+* (lanes 2 and 5) and *cps- porA::nspA* (lanes 1 and 6) recombinant *N. meningitidis* serogroupB strains and were analyzed under SDS-PAGE conditions in a 12% polyacrylamide gel. Gels were stained with Coomassie blue (lanes 1 to 3) or transferred to a nitrocellulose membrane and immuno-stained with an anti-PorA monoclonal antibody.

**Figure 5:** Analysis of NspA expression in protein extracts of recombinant *N. meningitidis* serogroupB strains (H44/76 derivatives). Proteins were extracted from whole bacteria (lanes 1 to 3) or outer-membrane blebs preparations (lanes 4 to 6) separated by SDS-PAGE on a 12% acrylamide gel and analyzed by immuno-blotting using an anti-NspA polyclonal serum. Samples corresponding to *cps*- (lanes 1 and 6), *cps- porA::pCMK+* (lanes 3 and 4) and *cps- porA::nspA* (lanes 2 and 5) were analyzed. Two forms of NspA were detected: a mature form (18kDa) co-migrating with the recombinant purified NspA, and a shorter form (15kDa).

**Figure 6:** Analysis of D15/omp85 expression in protein extracts of recombinant *N. meningitidis* serogroupB strains (H44/76 derivatives). Proteins were extracted from outer-membrane blebs preparations and were separated by SDS-PAGE on a 12% acrylamide gel and analyzed by immuno-blotting using an anti-omp85 polyclonal serum. Samples corresponding to *cps*- (lane 2), and *cps-, PorA+, pCMK+Omp85/D15* (lane 1) recombinant *N. meningitidis* serogroupB strains were analyzed.

**Figure 7:** General strategy for modulating gene expression by promoter delivery (RS stands for restriction site).

**Figure 8:** Analysis of outer-membrane blebs produced by recombinant *N. meningitidis* serogroupB *cps*- strains (H44/76 derivatives). Proteins were extracted from outer-membrane bleb preparations and were separated by SDS-PAGE under reducing conditions on a 4-20% gradient polyacrylamide gel. The gel was stained

with Coomassie brilliant blue R250. Lanes 2, 4, 6 corresponded to 5µg of total proteins whereas lanes 3, 5 and 7 were loaded with 10µg proteins.

5 **Figure 9:** Construction of a promoter replacement plasmid used to up-regulate the expression/production of Omp85/D15 in *Neisseria meningitidis* H44/76.

**Figure 10:** Analysis of OMP85 expression in total protein extracts of recombinant *NmB* (H44/76 derivatives). Gels were stained with Coomassie blue (A) or transferred to nitrocellulose membrane and immuno-stained with rabbit anti-OMP85 (*N.gono*) monoclonal antibody (B).  
10

**Figure 11:** Analysis of OMP85 expression in OMV preparations from recombinant *NmB* (H44/76 derivatives). Gels were stained with Coomassie blue (A) or transferred to nitrocellulose membrane and immuno-stained with rabbit anti-OMP85 polyclonal antibody (B).  
15

**Figure 12:** Schematic representation of the recombinant PCR strategy used to delete the *lacO* in the chimeric *porA/lacO* promoter.

20 **Figure 13:** Analysis of Hsf expression in total protein extracts of recombinant *N. meningitidis* serogroup B (H44/76 derivatives). Total proteins were recovered from Cps-PorA+(lanes 1), and Cps-PorA+/Hsf (lanes 2) recombinant *N. meningitidis* serogroup B strains and were analyzed under SDS-PAGE conditions in a 12% polyacrylamide gel. Gels were stained with Coomassie blue .

25 **Figure 14:** Analysis of GFP expression in total protein extracts of recombinant *N. meningitidis* (H44/76 derivative). Total protein were recovered from Cps-, PorA+ (lane1), Cps-, PorA- GFP+ (lane2 & 3) recombinant strains. Proteins were separated by PAGE-SDS in a 12% polyacrylamide gel and then stained with Coomassie blue.

30 **Figure 15:** Illustration of the pattern of major proteins on the surface of various recombinant bleb preparations as analysed by SDS-PAGE (Coomassie staining).

**Figure 16:** Specific anti-Hsf response for various bleb and recombinant bleb preparations using purified recombinant Hsf protein.

- 5 **Figure 17:** Analysis of NspA expression in total protein extracts of recombinant *NmB* (serogroup B derivatives). Gels were stained with Coomassie blue (A) or transferred to nitrocellulose membrane and immuno-stained with mouse anti-PorA monoclonal antibody (B) or mouse anti-NspA polyclonal antibody (C).

10

## DESCRIPTION OF THE INVENTION

The present invention relates to a general set of tools and methods capable of being used for manufacturing improved, genetically engineered blebs from Gram-negative bacterial strains. The invention includes methods used to make recombinant  
15 blebs more immunogenic, less toxic and safer for their use in a human and/or animal vaccine. Moreover, the present invention also describes specific methods necessary for constructing, producing, obtaining and using recombinant, engineered blebs from various Gram-negative bacteria, for vaccine, therapeutic and/or diagnostic purposes. By the methods of the invention, the biochemical composition of bacterial blebs can  
20 be manipulated by acting upon/altering the expression of bacterial genes encoding products present in or associated with bacterial outer-membrane blebs (outer membrane proteins or OMPs). The production of blebs using a method of genetic modification to increase, decrease or render conditional the expression of one or more genes encoding outer-membrane components are also included in the scope of this  
25 invention.

For clarity, the term "expression cassette" will refer herein to all the genetic elements necessary to express a gene or an operon and to produce and target the corresponding protein(s) of interest to outer-membrane blebs, derived from a given bacterial host. A non-exhaustive list of these features includes control elements  
30 (transcriptional and/or translational), protein coding regions and targeting signals, with appropriate spacing between them. Reference to the insertion of promoter sequences means, for the purposes of this invention, the insertion of a sequence with

at least a promoter function, and preferably one or more other genetic regulatory elements comprised within an expression cassette. Moreover, the term "integrative cassette" will refer herein to all the genetic elements required to integrate a DNA segment in given bacterial host. A non-exhaustive list of these features includes a delivery vehicle (or vector), with recombinogenic regions, and selectable and counter selectable markers.

Again for the purpose of clarity, the terms 'engineering a bacterial strain to produce less of said antigen' refers to any means to reduce the expression of an antigen of interest, relative to that of the non-modified (i.e., naturally occurring) bleb such that expression is at least 10% lower than that of the non-modified bleb. Preferably it is at least 50% lower. "Stronger promoter sequence" refers to a regulatory control element that increases transcription for a gene encoding antigen of interest. "Upregulating expression" refers to any means to enhance the expression of an antigen of interest, relative to that of the non-modified (i.e., naturally occurring) bleb. It is understood that the amount of 'upregulation' will vary depending on the particular antigen of interest but will not exceed an amount that will disrupt the membrane integrity of the bleb. Upregulation of an antigen refers to expression that is at least 10% higher than that of the non-modified bleb. Preferably it is at least 50% higher. More preferably it is at least 100% (2 fold) higher.

Aspects of the invention relate to individual methods for making improved engineered blebs, to a combination of such methods, and to the bleb compositions made as a result of these methods. Another aspect of the invention relates to the genetic tools used in order to genetically modify a chosen bacterial strain in order to extract improved engineered blebs from said strain.

The engineering steps of the processes of the invention can be carried out in a variety of ways known to the skilled person. For instance, sequences (e.g. promoters or open reading frames) can be inserted, and promoters/genes can be disrupted by the technique of transposon insertion. For instance, for upregulating a gene's expression, a strong promoter could be inserted via a transposon up to 2 kb upstream of the gene's initiation codon (more preferably 200-600 bp upstream, most preferably approximately 400 bp upstream). Point mutation or deletion may also be used (particularly for down-regulating expression of a gene).

Such methods, however, may be quite unstable or uncertain, and therefore it is preferred that the engineering step [particularly for processes a), b), c), d), e), h) and i) as described below] is performed via a homologous recombination event. Preferably, the event takes place between a sequence (a recombinogenic region) of at least 30 nucleotides on the bacterial chromosome, and a sequence (a second recombinogenic region) of at least 30 nucleotides on a vector transformed within the strain. Preferably the regions are 40-1000 nucleotides, more preferably 100-800 nucleotides, most preferably 500 nucleotides). These recombinogenic regions should be sufficiently similar that they are capable of hybridising to one another under highly stringent conditions (as defined later).

Recombination events may take place using a single recombinogenic region on chromosome and vector, or via a double cross-over event (with 2 regions on chromosome and vector). In order to perform a single recombination event, the vector should be a circular DNA molecule. In order to perform a double recombination event, the vector could be a circular or linear DNA molecule (see Figure 7). It is preferable that a double recombination event is employed and that the vector used is linear, as the modified bacterium so produced will be more stable in terms of reversion events. Preferably the two recombinogenic regions on the chromosome (and on the vector) are of similar (most preferably the same) length so as to promote double cross-overs. The double cross-over functions such that the two recombinogenic regions on the chromosome (separated by nucleotide sequence 'X') and the two recombinogenic regions on the vector (separated by nucleotide sequence 'Y') recombine to leave a chromosome unaltered except that X and Y have interchanged. The position of the recombinogenic regions can both be positioned upstream or downstream of, or may flank, an open reading frame of interest. These regions can consist of coding, non-coding, or a mixture of coding and non-coding sequence. The identity of X and Y will depend on the effect desired. X may be all or part of an open reading frame, and Y no nucleotides at all, which would result in sequence X being deleted from the chromosome. Alternatively Y may be a strong promoter region for insertion upstream of an open reading frame, and therefore X may be no nucleotides at all.

Suitable vectors will vary in composition depending what type of recombination event is to be performed, and what the ultimate purpose of the



recombination event is. Integrative vectors used to deliver region Y can be conditionally replicative or suicide plasmids, bacteriophages, transposons or linear DNA fragments obtained by restriction hydrolysis or PCR amplification. Selection of the recombination event is selected by means of selectable genetic marker such as  
5 genes conferring resistance to antibiotics (for instance kanamycin, erythromycin, chloramphenicol, or gentamycin), genes conferring resistance to heavy metals and/or toxic compounds or genes complementing auxotrophic mutations (for instance *pur*, *leu*, *met*, *aro*).

10

Process a) and f) – Down regulation/Removal of Variable and non-protective immunodominant antigens

Many surface antigens are variable among bacterial strains and as a consequence are protective only against a limited set of closely related strains. An  
15 aspect of this invention covers the reduction in expression, or, preferably, the deletion of the gene(s) encoding variable surface protein(s) which results in a bacterial strain producing blebs which, when administered in a vaccine, have a stronger potential for cross-reactivity against various strains due to a higher influence exerted by conserved proteins (retained on the outer membranes) on the vaccinee's immune system.  
20 Examples of such variable antigens include: for *Neisseria* - pili (PilC) which undergoes antigenic variations, PorA, Opa, TbpB, FrpB; for *H. influenzae* - P2, P5, pilin, IgA1-protease; and for *Moraxella* - CopB, OMP106.

Other types of gene that could be down-regulated or switched off are genes which, *in vivo*, can easily be switched on (expressed) or off by the bacterium. As outer  
25 membrane proteins encoded by such genes are not always present on the bacteria, the presence of such proteins in the bleb preparations can also be detrimental to the effectiveness of the vaccine for the reasons stated above. A preferred example to down-regulate or delete is *Neisseria* Opc protein. Anti-Opc immunity induced by an Opc containing bleb vaccine would only have limited protective capacity as the  
30 infecting organism could easily become Opc<sup>+</sup>. *H. influenzae* HgpA and HgpB are other examples of such proteins.

In process a), these variable or non-protective genes are down-regulated in expression, or terminally switched off. This has the above-mentioned surprising advantage of concentrating the immune system on better antigens that are present in low amounts on the outer surface of blebs.

5       The strain can be engineered in this way by a number of strategies including transposon insertion to disrupt the coding region or promoter region of the gene, or point mutations or deletions to achieve a similar result. Homologous recombination may also be used to delete a gene from a chromosome (where sequence X comprises part (preferably all) of the coding sequence of the gene of interest). It may additionally  
10 be used to change its strong promoter for a weaker (or no) promoter (where nucleotide sequence X comprises part (preferably all) of the promoter region of the gene, and nucleotide sequence Y comprises either a weaker promoter region [resulting in a decreased expression of the gene(s)/operon(s) of interest], or no promoter region). In this case it is preferable for the recombination event to occur within the region of the  
15 chromosome 1000 bp upstream of the gene of interest.

Alternatively, Y may confer a conditional transcriptional activity, resulting in a conditional expression of the gene(s)/operon(s) of interest (down-regulation). This is useful in the expression of molecules that are toxic to or not well supported by the bacterial host.

20       Most of the above-exemplified proteins are integral OMPs and their variability may be limited only to one or few of their surface exposed loops. Another aspect of this invention [process g)] covers the deletion of DNA regions coding for these surface exposed loops which leads to the expression of an integral OMP containing conserved surface exposed loops. Surface exposed loops of *H. influenzae* P2 and P5  
25 are preferred examples of proteins that could be transformed into cross-reactive antigens by using such a method. Again, homologous recombination is a preferred method of performing this engineering process.

Process b) - Promoter delivery and modulation:

30       A further aspect of the invention relates to modifying the composition of blebs by altering *in situ* the regulatory region controlling the expression of gene(s) and/or operon(s) of interest. This alteration may include partial or total replacement of the

endogenous promoter controlling the expression of a gene of interest, with one conferring a distinct transcriptional activity. This distinct transcriptional activity may be conferred by variants (point mutations, deletions and/or insertions) of the endogenous control regions, by naturally occurring or modified heterologous promoters or by a combination of both. Such alterations will preferably confer a transcriptional activity stronger than the endogenous one (introduction of a strong promoter), resulting in an enhanced expression of the gene(s)/operon(s) of interest (up-regulation). Such a method is particularly useful for enhancing the production of immunologically relevant Bleb components such as outer-membrane proteins and lipoproteins (preferably conserved OMPs, usually present in blebs at low concentrations).

Typical strong promoters that may be integrated in *Neisseria* are *porA* [SEQ ID NO: 24], *porB* [SEQ ID NO:26], *lgtF*, *Opa*, *p110*, *lst*, and *hpuAB*. *PorA* and *PorB* are preferred as constitutive, strong promoters. It has been established (Example 9) that the *PorB* promoter activity is contained in a fragment corresponding to nucleotides -1 to -250 upstream of the initiation codon of *porB*. In *Moraxella*, it is preferred to use the *ompH*, *ompG*, *ompE*, *OmpB1*, *ompB2*, *ompA*, *OMPCD* and *Omp106* promoters, and in *H. influenzae*, it is preferred to integrate the P2, P4, P1, P5 and P6 promoters.

Using the preferred double cross-over homologous recombination technology to introduce the promoter in the 1000 bp upstream region, promoters can be placed anywhere from 30-970 bp upstream of the initiation codon of the gene to be up-regulated. Although conventionally it is thought the promoter region should be relatively close to the open reading frame in order to obtain optimal expression of the gene, the present inventors have surprisingly found that placement of the promoter further away from the initiation codon results in large increases in expression levels. Thus it is preferred if the promoter is inserted 200-600 bp from the initiation codon of the gene, more preferably 300-500 bp, and most preferably approximately 400 bp from the initiation ATG.

Process c) - Bleb components produced conditionally

The expression of some genes coding for certain bleb components is carefully regulated. The production of the components is conditionally modulated and depends upon various metabolic and/or environmental signals. Such signals include, for example, iron-limitation, modulation of the redox potential, pH and temperature variations, nutritional changes. Some examples of bleb components known to be produced conditionally include iron-regulated outer-membrane proteins from *Neisseria* and *Moraxella* (for instance TbpB, LbpB), and substrate-inducible outer-membrane porins. The present invention covers the use of the genetic methods described previously (process a) or b)) to render constitutive the expression of such molecules. In this way, the influence of environmental signal upon the expression of gene(s) of interest can be overcome by modifying/replacing the gene's corresponding control region so that it becomes constitutively active (for instance by deleting part [preferably all] or the repressive control sequence – e.g. the operator region), or inserting a constitutive strong promoter. For iron regulated genes the *fur* operator may be removed. Alternatively, process i) may be used to deliver an additional copy of the gene/operon of interest in the chromosome which is placed artificially under the control of a constitutive promoter.

20

Processes d), and e) - Detoxification of LPS

The toxicity of bleb vaccines presents one of the largest problems in the use of blebs in vaccines. A further aspect of the invention relates to methods of genetically detoxifying the LPS present in Blebs. Lipid A is the primary component of LPS responsible for cell activation. Many mutations in genes involved in this pathway lead to essential phenotypes. However, mutations in the genes responsible for the terminal modifications steps lead to temperature-sensitive (*htrB*) or permissive (*msbB*) phenotypes. Mutations resulting in a decreased (or no) expression of these genes result in altered toxic activity of lipid A. Indeed, the non-lauroylated (*htrB* mutant) or non-myristoylated (*msbB* mutant) lipid A are less toxic than the wild-type lipid A. Mutations in the lipid A 4'-kinase encoding gene (*lpxK*) also decreases the toxic activity of lipid A.

30

Process d) thus involves either the deletion of part (or preferably all) of one or more of the above open reading frames or promoters. Alternatively, the promoters could be replaced with weaker promoters. Preferably the homologous recombination techniques described above are used to carry out the process.

5 The sequences of the *htrB* and *msbB* genes from *Neisseria meningitidis* B, *Moraxella catarrhalis*, and *Haemophilus influenzae* are additionally provided for this purpose.

LPS toxic activity could also be altered by introducing mutations in genes/loci involved in polymyxin B resistance (such resistance has been correlated with addition  
10 of aminoarabinose on the 4' phosphate of lipid A). These genes/loci could be *pmrE* that encodes a UDP-glucose dehydrogenase, or a region of antimicrobial peptide-resistance genes common to many enterobacteriaceae which could be involved in aminoarabinose synthesis and transfer. The gene *pmrF* that is present in this region encodes a dolicol-phosphate manosyl transferase (Gunn J.S., Kheng, B.L., Krueger J.,  
15 Kim K., Guo L., Hackett M., Miller S.I. 1998. *Mol. Microbiol.* 27: 1171-1182).

Mutations in the PhoP-PhoQ regulatory system, which is a phospho-relay two component regulatory system (f. i. PhoP constitutive phenotype, PhoP<sup>c</sup>), or low Mg<sup>++</sup> environmental or culture conditions (that activate the PhoP-PhoQ regulatory system) lead to the addition of aminoarabinose on the 4'-phosphate and 2-hydroxymyristate  
20 replacing myristate (hydroxylation of myristate). This modified lipid A displays reduced ability to stimulate E-selectin expression by human endothelial cells and TNF- $\alpha$  secretion from human monocytes.

Process e) involves the upregulation of these genes using a strategy as described above (strong promoters being incorporated, preferably using homologous  
25 recombination techniques to carry out the process).

Alternatively, rather than performing any such mutation, a polymyxin B resistant strain could be used as a vaccine production strain (in conjunction with one or more of the other processes of the invention), as blebs from such strains also have reduced LPS toxicity (for instance as shown for meningococcus - van der Ley, P,  
30 Hamstra, HJ, Kramer, M, Steeghs, L, Petrov, A and Poolman, JT. 1994. *In*: Proceedings of the ninth international pathogenic *Neisseria* conference. The Guildhall, Winchester, England).

As a further alternative (and further aspect of the invention) the inventors provide a method of detoxifying a Gram-negative bacterial strain comprising the step of culturing the strain in a growth medium containing 0.1mg-100g of aminoarabinose per litre medium.

5 As a further still alternative, synthetic peptides that mimic the binding activity of polymyxin B (described below) may be added to the Bleb preparation in order to reduce LPS toxic activity (Rustici, A, Velucchi, M, Faggioni, R, Sironi, M, Ghezzi, P, Quataert, S, Green, B and Porro M 1993. *Science* 259: 361-365; Velucchi, M, Rustici, A, Meazza, C, Villa, P, Ghezzi, P and Porro, M. 1997. *J. Endotox. Res.* 4:).

10 Process f) - Anchoring homologous or heterologous proteins to outer-membrane blebs whilst reducing the toxicity of LPS

A further aspect of this invention covers the use of genetic sequences encoding polymyxin B peptides (or analogues thereof) as a means to target fusion proteins to the outer-membrane. Polymyxin B is a cyclic peptide composed of non tRNA-  
15 encoded amino acids (produced by Gram-positive actinomycetal organisms) that binds very strongly to the Lipid A part of LPS present in the outer-membrane. This binding decreases the intrinsic toxicity of LPS (endotoxin activity). Peptides mimicking the structure of Polymyxin B and composed of canonical (tRNA encoded) amino acids have been developed and also bind lipid A with a strong affinity. These  
20 peptides have been used for detoxifying LPS. One of these peptides known as SAEP-2 (Nterminus-Lys-Thr-Lys-Cys-Lys-Phe-Leu-Lys-Lys-Cys-Cterminus) was shown to be very promising in that respect (Molecular Mapping and detoxifying of the Lipid A binding site by synthetic peptides (1993). Rustici, A., Velucchi, M., Faggioni, R., Sironi, M., Ghezzi, P., Quataert, S., Green, B. and M. Porro. *Science* 259, 361-365).  
25

The present process f) of the invention provides an improvement of this use. It has been found that the use of DNA sequences coding for the SEAP-2 peptide (or derivatives thereof), fused genetically to a gene of interest (encoding for instance a T cell antigen or a protective antigen that is usually secreted such as a toxin, or a  
30 cytosolic or periplasmic protein) is a means for targeting the corresponding recombinant protein to the outer-membrane of a preferred bacterial host (whilst at the same time reducing the toxicity of the LPS).

This system is suitable for labile proteins which would not be directly exposed to the outside of the bleb. The bleb would therefore act as a delivery vehicle which would expose the protein to the immune system once the blebs had been engulfed by T-cells. Alternatively, the genetic fusion should also comprise a signal peptide or transmembrane domain such that the recombinant protein may cross the outer membrane for exposure to the host's immune system.

This targeting strategy might be of particular interest in the case of genes encoding proteins that are not normally targeted to the outer-membrane. This methodology also allows the isolation of recombinant blebs enriched in the protein of interest. Preferably, such a peptide targeting signal allows the enrichment of outer membrane blebs in one or several proteins of interest, which are naturally not found in that given subcellular localization. A non exhaustive list of bacteria that can be used as a recipient host for such a production of recombinant blebs includes *Neisseria meningitidis*, *Neisseiria gonorrhoeae*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Pseudomonas aeruginosa*, *Chlamydia trachomatis*, and *Chlamydia pneumoniae*.

Although it is preferred that the gene for the construct is engineered into the chromosome of the bacterium [using process i)], an alternative preferred embodiment is for SAEP-2-tagged recombinant proteins to be made independently, and attached at a later stage to a bleb preparation.

A further embodiment is the use of such constructs in a method of protein purification. The system could be used as part of an expression system for producing recombinant proteins in general. The SAEP-2 peptide tag can be used for affinity purification of the protein to which it is attached using a column containing immobilised lipid A molecules.

25

#### Process h) - Cross-reactive polysaccharides

The isolation of bacterial outer-membrane blebs from encapsulated Gram-negative bacteria often results in the co-purification of capsular polysaccharide. In some cases, this "contaminant" material may prove useful since polysaccharide may enhance the immune response conferred by other bleb components. In other cases however, the presence of contaminating polysaccharide material in bacterial bleb preparations may prove detrimental to the use of the blebs in a vaccine. For instance,

30

it has been shown at least in the case of *N. meningitidis* that the serogroup B capsular polysaccharide does not confer protective immunity and is susceptible to induce an adverse auto-immune response in humans. Consequently, process h) of the invention is the engineering of the bacterial strain for bleb production such that it is free of capsular polysaccharide. The blebs will then be suitable for use in humans. A particularly preferred example of such a bleb preparation is one from *N. meningitidis* serogroup B devoid of capsular polysaccharide.

This may be achieved by using modified bleb production strains in which the genes necessary for capsular biosynthesis and/or export have been impaired. Inactivation of the gene coding for capsular polysaccharide biosynthesis or export can be achieved by mutating (point mutation, deletion or insertion) either the control region, the coding region or both (preferably using the homologous recombination techniques described above). Moreover, inactivation of capsular biosynthesis genes may also be achieved by antisense over-expression or transposon mutagenesis. A preferred method is the deletion of some or all of the *Neisseria meningitidis cps* genes required for polysaccharide biosynthesis and export. For this purpose, the replacement plasmid pMF121 (described in Frosh et al.1990, *Mol. Microbiol.* 4:1215-1218) can be used to deliver a mutation deleting the *cpsCAD* (+ *galE*) gene cluster. Alternatively the *siaD* gene could be deleted, or down-regulated in expression (the meningococcal *siaD* gene encodes alpha-2,3-sialyltransferase, an enzyme required for capsular polysaccharide and LOS synthesis). Such mutations may also remove host-similar structures on the saccharide portion of the LPS of the bacteria.

Process i) - Delivery of one or more further copies of a Gene and/or operon in a host chromosome, or delivery of a heterologous gene and/or operon in a host chromosome.

An efficient strategy to modulate the composition of a Bleb preparation is to deliver one or more copies of a DNA segment containing an expression cassette into the genome of a Gram-negative bacterium. A non exhaustive list of preferred bacterial species that could be used as a recipient for such a cassette includes *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Pseudomonas aeruginosa*, *Chlamydia trachomatis*, *Chlamydia pneumoniae*. The gene(s) contained in the expression cassette may be homologous (or



endogenous) (i.e. exist naturally in the genome of the manipulated bacterium) or heterologous (i.e. do not exist naturally in the genome of the manipulated bacterium). The reintroduced expression cassette may consist of unmodified, "natural" promoter/gene/operon sequences or engineered expression cassettes in which the promoter region and/or the coding region or both have been altered. A non-exhaustive list of preferred promoters that could be used for expression includes the promoters *porA*, *porB*, *lbpB*, *tbpB*, *p110*, *lst*, *hpuAB* from *N. meningitidis* or *N. gonorrhoeae*, the promoters *p2*, *p5*, *p4*, *ompF*, *p1*, *ompH*, *p6*, *hin47* from *H. influenzae*, the promoters *ompH*, *ompG*, *ompCD*, *ompE*, *ompB1*, *ompB2*, *ompA* of *M. catarrhalis*, the promoter  $\lambda$ pL, *lac*, *tac*, *araB* of *Escherichia coli* or promoters recognized specifically by bacteriophage RNA polymerase such as the *E. coli* bacteriophage T7. A non-exhaustive list of preferred genes that could be expressed in such a system includes *Neisseria* NspA, Omp85, PilQ, TbpA/B complex, Hsf, PldA, HasR; *Chlamydia* MOMP, HMWP; *Moraxella* OMP106, HasR, PilQ, OMP85, PldA; *Bordetella pertussis* FHA, PRN, PT.

In a preferred embodiment of the invention the expression cassette is delivered and integrated in the bacterial chromosome by means of homologous and/or site specific recombination. Integrative vectors used to deliver such genes and/or operons can be conditionally replicative or suicide plasmids, bacteriophages, transposons or linear DNA fragments obtained by restriction hydrolysis or PCR amplification. Integration is preferably targeted to chromosomal regions dispensable for growth *in vitro*. A non exhaustive list of preferred loci that can be used to target DNA integration includes the *porA*, *porB*, *opa*, *opc*, *rmp*, *omp26*, *lecA*, *cps*, *lgtB* genes of *Neisseria meningitidis* and *Neisseria gonorrhoeae*, the *P1*, *P5*, *hmw1/2*, *IgA-protease*, *fimE* genes of NTHi; the *lecA1*, *lecA2*, *omp106*, *uspA1*, *uspA2* genes of *Moraxella catarrhalis*. Alternatively, the expression cassette used to modulate the expression of bleb component(s) can be delivered into a bacterium of choice by means of episomal vectors such as circular/linear replicative plasmids, cosmids, phasmids, lysogenic bacteriophages or bacterial artificial chromosomes. Selection of the recombination event can be selected by means of selectable genetic marker such as genes conferring resistance to antibiotics (for instance kanamycin, erythromycin, chloramphenicol, or gentamycin), genes conferring resistance to heavy metals and/or

toxic compounds or genes complementing auxotrophic mutations (for instance *pur*, *leu*, *met*, *aro*).

*Heterologous Genes - Expression of foreign proteins in outer-membrane blebs*

5 Outer-membrane bacterial blebs represent a very attractive system to produce, isolate and deliver recombinant proteins for vaccine, therapeutic and/or diagnostic uses. A further aspect of this invention is in respect of the expression, production and targeting of foreign, heterologous proteins to the outer-membrane, and the use of the bacteria to produce recombinant blebs.

10 A preferred method of achieving this is via a process comprising the steps of: introducing a heterologous gene, optionally controlled by a strong promoter sequence, into the chromosome of a Gram-negative strain by homologous recombination. Blebs may be made from the resulting modified strain.

A non-exhaustive list of bacteria that can be used as a recipient host for  
15 production of recombinant blebs includes *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Pseudomonas aeruginosa*, *Chlamydia trachomatis*, *Chlamydia pneumoniae*. The gene expressed in such a system can be of viral, bacterial, fungal, parasitic or higher eukaryotic origin.

A preferred application of the invention includes a process for the expression  
20 of *Moraxella*, *Haemophilus* and/or *Pseudomonas* outer-membrane proteins (integral, polytopic and/or lipoproteins) in *Neisseria meningitidis* recombinant blebs. The preferable integration loci are stated above, and genes that are preferably introduced are those that provide protection against the bacterium from which they were isolated. Preferred protective genes for each bacterium are described below.

25 Further preferred applications are: blebs produced from a modified *Haemophilus influenzae* strain where the heterologous gene is a protective OMP from *Moraxella catarrhalis*; and blebs produced from a modified *Moraxella catarrhalis* strain where the heterologous gene is a protective OMP from *Haemophilus influenzae* (preferred loci for gene insertion are given above, and preferred protective antigens  
30 are described below).

A particularly preferred application of this aspect is in the field of the prophylaxis or treatment of sexually-transmitted diseases (STDs). It is often

difficult for practitioners to determine whether the principal cause of a STD is due to gonococcus or *Chlamydia trachomatis* infection. These two organisms are the main causes of salpingitis – a disease which can lead to sterility in the host. It would therefore be useful if a STD could be vaccinated against or treated with a combined vaccine effective against disease caused by both organisms. The Major Outer Membrane Protein (MOMP) of *C. trachomatis* has been shown to be the target of protective antibodies. However, the structural integrity of this integral membrane protein is important for inducing such antibodies. In addition, the epitopes recognised by these antibodies are variable and define more than 10 serovars. The previously described aspect of this invention allows the proper folding of one or more membrane proteins within a bleb outer membrane preparation. The engineering of a gonococcal strain expressing multiple *C. trachomatis* MOMP serovars in the outer membrane, and the production of blebs therefrom, produces a single solution to the multiple problems of correctly folded membrane proteins, the presentation of sufficient MOMP serovars to protect against a wide spectrum of serovars, and the simultaneous prophylaxis/treatment of gonococcal infection (and consequently the non-requirement of practitioners to initially decide which organism is causing particular clinical symptoms – both organisms can be vaccinated against simultaneously thus allowing the treatment of the STD at a very early stage). Preferred loci for gene insertion in the gonococcal chromosome are give above. Other preferred, protective *C. trachomatis* genes that could be incorporated are HMWP, PmpG and those OMPs disclosed in WO 99/28475.

*Targeting of heterologous proteins to outer-membrane blebs:*

The expression of some heterologous proteins in bacterial blebs may require the addition of outer-membrane targeting signal(s). The preferred method to solve this problem is by creating a genetic fusion between a heterologous gene and a gene coding for a resident OMP as a specific approach to target recombinant proteins to blebs. Most preferably, the heterologous gene is fused to the signal peptides sequences of such an OMP.

Neisserial bleb preparations

One or more of the following genes (encoding protective antigens) are preferred for upregulation via processes b) and/or i) when carried out on a Neisserial strain, including gonococcus, and meningococcus (particularly *N. meningitidis* B):

5 NspA (WO 96/29412), Hsf-like (WO 99/31132), Hap (PCT/EP99/02766), PorA, PorB, OMP85 (WO 00/23595), PilQ (PCT/EP99/03603), PldA (PCT/EP99/06718), FrpB (WO 96/31618), TbpA (US 5,912,336), TbpB, FrpA/FrpC (WO 92/01460), LbpA/LbpB (PCT/EP98/05117), FhaB (WO 98/02547), HasR (PCT/EP99/05989), lipo02 (PCT/EP99/08315), Tbp2 (WO 99/57280), MltA (WO 99/57280), and ctrA

10 (PCT/EP00/00135). They are also preferred as genes which may be heterologously introduced into other Gram-negative bacteria.

One or more of the following genes are preferred for downregulation via process a): PorA, PorB, PilC, TbpA, TbpB, LbpA, LbpB, Opa, and Opc.

One or more of the following genes are preferred for downregulation via

15 process d): htrB, msbB and lpxK.

One or more of the following genes are preferred for upregulation via process e): pmrA, pmrB, pmrE, and pmrF.

Preferred repressive control sequences for process c) are: the *fur* operator region (particularly for either or both of the TbpB or LbpB genes); and the DtxR

20 operator region.

One or more of the following genes are preferred for downregulation via process h): galE, siaA, siaB, siaC, siaD, ctrA, ctrB, ctrC, and ctrD.

*Pseudomonas aeruginosa* bleb preparations

25 One or more of the following genes (encoding protective antigens) are preferred for upregulation via processes b) and/or i): PcrV, OprF, OprI. They are also preferred as genes which may be heterologously introduced into other Gram-negative bacteria.

*Moraxella catarrhalis* bleb preparations

30 One or more of the following genes (encoding protective antigens) are preferred for upregulation via processes b) and/or i): OMP106 (WO 97/41731 & WO

96/34960), HasR (PCT/EP99/03824), PilQ (PCT/EP99/03823), OMP85 (PCT/EP00/01468), lipo06 (GB 9917977.2), lipo10 (GB 9918208.1), lipo11 (GB 9918302.2), lipo18 (GB 9918038.2), P6 (PCT/EP99/03038), ompCD, CopB (Helminen ME, et al (1993) Infect. Immun. 61:2003-2010), D15 (PCT/EP99/03822),  
 5 OmpLA1 (PCT/EP99/06781), Hly3 (PCT/EP99/03257), LbpA and LbpB (WO 98/55606), TbpA and TbpB (WO 97/13785 & WO 97/32980), OmpE, UspA1 and UspA2 (WO 93/03761), and Omp21. They are also preferred as genes which may be heterologously introduced into other Gram-negative bacteria.

One or more of the following genes are preferred for downregulation via  
 10 process a): CopB, OMP106, OmpB1, TbpA, TbpB, LbpA, and LbpB.

One or more of the following genes are preferred for downregulation via process d): htrB, msbB and lpxK.

One or more of the following genes are preferred for upregulation via process  
 15 e): pmrA, pmrB, pmrE, and pmrF.

#### *Haemophilus influenzae* bleb preparations

One or more of the following genes (encoding protective antigens) are preferred for upregulation via processes b) and/or i): D15 (WO 94/12641), P6 (EP 281673), TbpA, TbpB, P2, P5 (WO 94/26304), OMP26 (WO 97/01638), HMW1,  
 20 HMW2, HMW3, HMW4, Hia, Hsf, Hap, Hin47, and Hif (all genes in this operon should be upregulated in order to upregulate pilin). They are also preferred as genes which may be heterologously introduced into other Gram-negative bacteria.

One or more of the following genes are preferred for downregulation via  
 25 process a): P2, P5, Hif, IgA1-protease, HgpA, HgpB, HMW1, HMW2, Hxu, TbpA, and TbpB.

One or more of the following genes are preferred for downregulation via process d): htrB, msbB and lpxK.

One or more of the following genes are preferred for upregulation via process  
 30 e): pmrA, pmrB, pmrE, and pmrF.

### Vaccine Formulations

A preferred embodiment of the invention is the formulation of the bleb preparations of the invention in a vaccine which may also comprise a pharmaceutically acceptable excipient.

5       The manufacture of bleb preparations from any of the aforementioned modified strains may be achieved by any of the methods well known to a skilled person. Preferably the methods disclosed in EP 301992, US 5,597,572, EP 11243 or US 4,271,147 are used. Most preferably, the method described in Example 8 is used.

10       Vaccine preparation is generally described in Vaccine Design ("The subunit and adjuvant approach" (eds Powell M.F. & Newman M.J.) (1995) Plenum Press New York).

15       The bleb preparations of the present invention may be adjuvanted in the vaccine formulation of the invention. Suitable adjuvants include an aluminium salt such as aluminum hydroxide gel (alum) or aluminium phosphate, but may also be a salt of calcium (particularly calcium carbonate), iron or zinc, or may be an insoluble suspension of acylated tyrosine, or acylated sugars, cationically or anionically derivatised polysaccharides, or polyphosphazenes.

20       Suitable Th1 adjuvant systems that may be used include, Monophosphoryl lipid A, particularly 3-de-O-acylated monophosphoryl lipid A, and a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL) together with an aluminium salt. An enhanced system involves the combination of a monophosphoryl lipid A and a saponin derivative particularly the combination of QS21 and 3D-MPL as disclosed in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol as disclosed in WO96/33739. A particularly potent adjuvant formulation involving QS21 3D-MPL and tocopherol in an oil in water emulsion is described in WO95/17210 and is a preferred formulation.

25       The vaccine may comprise a saponin, more preferably QS21. It may also comprise an oil in water emulsion and tocopherol. Unmethylated CpG containing oligo nucleotides (WO 96/02555) are also preferential inducers of a TH1 response and are suitable for use in the present invention.

30       The vaccine preparation of the present invention may be used to protect or treat a mammal susceptible to infection, by means of administering said vaccine via

systemic or mucosal route. These administrations may include injection *via* the intramuscular, intraperitoneal, intradermal or subcutaneous routes; or *via* mucosal administration to the oral/alimentary, respiratory, genitourinary tracts. Thus one aspect of the present invention is a method of immunizing a human host against a disease caused by infection of a gram-negative bacteria, which method comprises administering to the host an immunoprotective dose of the bleb preparation of the present invention.

The amount of antigen in each vaccine dose is selected as an amount which induces an immunoprotective response without significant, adverse side effects in typical vaccinees. Such amount will vary depending upon which specific immunogen is employed and how it is presented. Generally, it is expected that each dose will comprise 1-100 $\mu$ g of protein antigen, preferably 5-50 $\mu$ g, and most typically in the range 5 - 25 $\mu$ g.

An optimal amount for a particular vaccine can be ascertained by standard studies involving observation of appropriate immune responses in subjects. Following an initial vaccination, subjects may receive one or several booster immunisations adequately spaced.

#### Ghost or Killed Whole cell vaccines

The inventors envisage that the above improvements to bleb preparations and vaccines can be easily extended to ghost or killed whole cell preparations and vaccines (with identical advantages). The modified Gram-negative strains of the invention from which the bleb preparations are made can also be used to make ghost and killed whole cell preparations. Methods of making ghost preparations (empty cells with intact envelopes) from Gram-negative strains are well known in the art (see for example WO 92/01791). Methods of killing whole cells to make inactivated cell preparations for use in vaccines are also well known. The terms 'bleb preparations' and 'bleb vaccines' as well as the processes described throughout this document are therefore applicable to the terms 'ghost preparation' and 'ghost vaccine', and 'killed whole cell preparation' and 'killed whole cell vaccine', respectively, for the purposes of this invention.

Combinations of methods a) – i)

It may be appreciated that one or more of the above processes may be used to produce a modified strain from which to make improved bleb preparations of the invention. Preferably one such process is used, more preferably two or more (2, 3, 4, 5, 6, 7, 8 or 9) of the processes are used in order to manufacture the bleb vaccine. As each additional method is used in the manufacture of the bleb vaccine, each improvement works in conjunction with the other methods used in order to make an optimised engineered bleb preparation.

A preferred meningococcal (particularly *N. meningitidis* B) bleb preparation comprises the use of processes a), b), d) and/or e), and h). Such bleb preparations are safe (no structures similar to host structures), non-toxic, and structured such that the host immune response will be focused on high levels of protective (and preferably conserved) antigens. All the above elements work together in order to provide an optimised bleb vaccine.

Similarly for *M. catarrhalis* and non-typeable *H. influenzae*, preferred bleb preparations comprise the use of processes a), b), and d) and/or e).

A further aspect of the invention is thus an immuno-protective and non-toxic Gram-negative bleb, ghost, or killed whole cell vaccine suitable for paediatric use.

By paediatric use it is meant use in infants less than 4 years old.

By immunoprotective it is meant that at least 40% (and preferably 50, 60, 70, 80, 90 and 100%) of infants seroconvert (4-fold increase in bactericidal activity [the dilution of antisera at which 50% of bacteria die – see for example PCT/EP98/05117]) against a set of heterologous strains to be selected from the major clonal groups known. For meningococcus B these strains should have a different PorA type from the bleb production strain, and should preferably be 2, 3, 4 or, most preferably, all 5 of strains H44/76, M97/252078, BZ10, NGP165 and CU385. For non-typeable *H. influenzae*, the strains should preferably be 2, 3, 4 or, most preferably, all 5 of strains 3224A, 3219C, 3241A, 640645, and A840177. For *M. catarrhalis*, the strains should preferably be 2, 3, 4 or, most preferably, all 5 of strains ATCC 43617, 14, 358, 216 and 2926.



By non-toxic it is meant that there is a significant (2-4 fold, preferably 10 fold) decrease of endotoxin activity as measured by the well-known LAL and pyrogenicity assays.

## 5 Vaccine Combinations

A further aspect of the invention are vaccine combinations comprising the bleb preparations of the invention with other antigens which are advantageously used against certain disease states. It has been found that blebs are particularly suitable for formulating with other antigens, as they advantageously have an adjuvant effect on the  
10 antigens they are mixed with.

In one preferred combination, the meningococcus B bleb preparations of the invention are formulated with 1, 2, 3 or preferably all 4 of the following meningococcal capsular polysaccharides which may be plain or conjugated to a protein carrier: A, C, Y or W. Such a vaccine may be advantageously used as a global  
15 meningococcus vaccine. Rather than use the meningococcus B bleb preparations of the invention, it is also envisaged that the formulation could alternatively contain wild-type meningococcus B bleb preparations from 2 or more (preferably several) strains belonging to several subtype/serotypes (for instance chosen from P1.15, P1.7,16, P1.4, and P1.2).

20 In a further preferred embodiment, the meningococcus B bleb preparations of the invention [or the aforementioned mix of 2 or more wild-type meningococcus B bleb preparations], preferably formulated with 1, 2, 3 or all 4 of the plain or conjugated meningococcal capsular polysaccharides A, C, Y or W, are formulated with a conjugated *H. influenzae* b capsular polysaccharide, and one or more plain or  
25 conjugated pneumococcal capsular polysaccharides. Optionally, the vaccine may also comprises one or more protein antigens that can protect a host against *Streptococcus pneumoniae* infection. Such a vaccine may be advantageously used as a global meningitis vaccine.

The pneumococcal capsular polysaccharide antigens are preferably selected  
30 from serotypes 1, 2, 3, 4, 5, 6B, 7F, 8, 9N, 9V, 10A, 11A, 12F, 14, 15B, 17F, 18C, 19A, 19F, 20, 22F, 23F and 33F (most preferably from serotypes 1, 3, 4, 5, 6B, 7F, 9V, 14, 18C, 19F and 23F).

Preferred pneumococcal proteins antigens are those pneumococcal proteins which are exposed on the outer surface of the pneumococcus (capable of being recognised by a host's immune system during at least part of the life cycle of the pneumococcus), or are proteins which are secreted or released by the pneumococcus.

5 Most preferably, the protein is a toxin, adhesin, 2-component signal transducer, or lipoprotein of *Streptococcus pneumoniae*, or fragments thereof. Particularly preferred proteins include, but are not limited to: pneumolysin (preferably detoxified by chemical treatment or mutation) [Mitchell *et al.* Nucleic Acids Res. 1990 Jul 11; 18(13): 4010 "Comparison of pneumolysin genes and proteins from *Streptococcus*

10 *pneumoniae* types 1 and 2.", Mitchell *et al.* Biochim Biophys Acta 1989 Jan 23; 1007(1): 67-72 "Expression of the pneumolysin gene in *Escherichia coli*: rapid purification and biological properties.", WO 96/05859 (A. Cyanamid), WO 90/06951 (Paton *et al.*), WO 99/03884 (NAVA)]; PspA and transmembrane deletion variants thereof (US 5804193 - Briles *et al.*); PspC and transmembrane deletion variants

15 thereof (WO 97/09994 - Briles *et al.*); PsaA and transmembrane deletion variants thereof (Berry & Paton, Infect Immun 1996 Dec;64(12):5255-62 "Sequence heterogeneity of PsaA, a 37-kilodalton putative adhesin essential for virulence of *Streptococcus pneumoniae*"); pneumococcal choline binding proteins and transmembrane deletion variants thereof; CbpA and transmembrane deletion variants

20 thereof (WO 97/41151; WO 99/51266); Glyceraldehyde-3-phosphate - dehydrogenase (Infect. Immun. 1996 64:3544); HSP70 (WO 96/40928); PcpA (Sanchez-Beato *et al.* FEMS Microbiol Lett 1998, 164:207-14); M like protein, SB patent application No. EP 0837130; and adhesin 18627, SB Patent application No. EP 0834568. Further preferred pneumococcal protein antigens are those disclosed in WO

25 98/18931, particularly those selected in WO 98/18930 and PCT/US99/30390.

In a further preferred embodiment, the *Moraxella catarrhalis* bleb preparations of the invention are formulated with one or more plain or conjugated pneumococcal capsular polysaccharides, and one or more antigens that can protect a host against non-typeable *H. influenzae* infection. Optionally, the vaccine may also comprise one

30 or more protein antigens that can protect a host against *Streptococcus pneumoniae* infection. The vaccine may also optionally comprise one or more antigens that can protect a host against RSV and/or one or more antigens that can protect a host against

influenza virus. Such a vaccine may be advantageously used as a global otitis media vaccine.

Preferred non-typeable *H. influenzae* protein antigens include Fimbrin protein (US 5766608) and fusions comprising peptides therefrom (eg LB1 Fusion) (US 5843464 - Ohio State Research Foundation), OMP26, P6, protein D, TbpA, TbpB, Hia, Hmw1, Hmw2, Hap, and D15.

Preferred influenza virus antigens include whole, live or inactivated virus, split influenza virus, grown in eggs or MDCK cells, or Vero cells or whole flu virosomes (as described by R. Gluck, Vaccine, 1992, 10, 915-920) or purified or recombinant proteins thereof, such as HA, NP, NA, or M proteins, or combinations thereof.

Preferred RSV (Respiratory Syncytial Virus) antigens include the F glycoprotein, the G glycoprotein, the HN protein, or derivatives thereof.

In a still further preferred embodiment, the non-typeable *H. influenzae* bleb preparations of the invention are formulated with one or more plain or conjugated pneumococcal capsular polysaccharides, and one or more antigens that can protect a host against *M. catarrhalis* infection. Optionally, the vaccine may also comprise one or more protein antigens that can protect a host against *Streptococcus pneumoniae* infection. The vaccine may also optionally comprise one or more antigens that can protect a host against RSV and/or one or more antigens that can protect a host against influenza virus. Such a vaccine may be advantageously used as a global otitis media vaccine.

#### Nucleotide sequences of the invention

A further aspect of the invention relates to the provision of new nucleotide sequences which may be used in the processes of the invention. Specific upstream regions from various genes from various strains are provided which can be used in, for instance, processes a), b), d) and h). In addition, coding regions are provided for performing process d).

*General method for the analysis of the non-coding flanking region of a bacterial gene, and its exploitation for modulated expression of the gene in blebs*

The non-coding flanking regions of a specific gene contain regulatory elements important in the expression of the gene. This regulation takes place both at the transcriptional and translational level. The sequence of these regions, either upstream or downstream of the open reading frame of the gene, can be obtained by DNA sequencing. This sequence information allows the determination of potential regulatory motifs such as the different promoter elements, terminator sequences, inducible sequence elements, repressors, elements responsible for phase variation, the Shine-Dalgarno sequence, regions with potential secondary structure involved in regulation, as well as other types of regulatory motifs or sequences.

This sequence information allows the modulation of the natural expression of the gene in question. The upregulation of the gene expression may be accomplished by altering the promoter, the Shine-Dalgarno sequence, potential repressor or operator elements, or any other elements involved. Likewise, downregulation of expression can be achieved by similar types of modifications. Alternatively, by changing phase variation sequences, the expression of the gene can be put under phase variation control, or may be uncoupled from this regulation. In another approach, the expression of the gene can be put under the control of one or more inducible elements allowing regulated expression. Examples of such regulation includes, but is not limited to, induction by temperature shift, addition of inductor substrates like selected carbohydrates or their derivatives, trace elements, vitamins, co-factors, metal ions, etc.

Such modifications as described above can be introduced by several different means. The modification of sequences involved in gene expression can be done *in vivo* by random mutagenesis followed by selection for the desired phenotype. Another approach consists in isolating the region of interest and modifying it by random mutagenesis, or site-directed replacement, insertion or deletion mutagenesis. The modified region can then be reintroduced into the bacterial genome by homologous recombination, and the effect on gene expression can be assessed. In another approach, the sequence knowledge of the region of interest can be used to replace or delete all or part of the natural regulatory sequences. In this case, the regulatory region targeted is isolated and modified so as to contain the regulatory elements from another gene, a combination of regulatory elements from different genes, a synthetic regulatory region, or any other regulatory region, or to delete selected parts of the

wild-type regulatory sequences. These modified sequences can then be reintroduced into the bacterium via homologous recombination into the genome.

In process b), for example, the expression of a gene can be modulated by exchanging its promoter with a stronger promoter (through isolating the upstream  
5 sequence of the gene, in vitro modification of this sequence, and reintroduction into the genome by homologous recombination). Upregulated expression can be obtained in both the bacterium as well as in the outer membrane vesicles shed (or made) from the bacterium.

In other preferred examples, the described approaches can be used to generate  
10 recombinant bacterial strains with improved characteristics for vaccine applications, as described above. These can be, but are not limited to, attenuated strains, strains with increased expression of selected antigens, strains with knock-outs (or decreased expression) of genes interfering with the immune response, and strains with modulated expression of immunodominant proteins.

15  
SEQ ID NO:2-23, 25, 27-38 are all Neisserial upstream sequences (upstream of the initiation codon of various preferred genes) comprising approximately 1000 bp each. SEQ ID NO: 39-62 are all *M. catarrhalis* upstream sequences (upstream of the initiation codon of various preferred genes) comprising approximately 1000 bp each.  
20 SEQ ID NO: 63-75 are all *H. influenzae* upstream sequences (upstream of the initiation codon of various preferred genes) comprising approximately 1000 bp each. All of these can be used in genetic methods (particularly homologous recombination) for up-regulating, or down-regulating the open reading frames to which they are associated (as described before). SEQ ID NO: 76-81 are the coding regions for the  
25 HtrB and MsbB genes from Neisseria, *M. catarrhalis*, and *Haemophilus influenzae*. These can be used in genetic methods (particularly homologous recombination) for down-regulating (in particular deleting) part (preferably all) of these genes [process d)].

Another aspect of the invention is thus an isolated polynucleotide sequence  
30 which hybridises under highly stringent conditions to at least a 30 nucleotide portion of the nucleotides in SEQ ID NO: 2-23, 25, 27-81 or a complementary strand thereof. Preferably the isolated sequence should be long enough to perform homologous

recombination with the chromosomal sequence if it is part of a suitable vector – namely at least 30 nucleotides (preferably at least 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, or 500 nucleotides). More preferably the isolated polynucleotide should comprise at least 30 nucleotides (preferably at least 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, or 500 nucleotides) of SEQ ID NO: 2-23, 25, 27-81 or a complementary strand thereof.

As used herein, highly stringent hybridization conditions include, for example, 6X SSC, 5X Denhardt, 0.5% SDS, and 100 µg/mL fragmented and denatured salmon sperm DNA hybridized overnight at 65 °C and washed in 2X SSC, 0.1% SDS one time at room temperature for about 10 minutes followed by one time at 65 °C for about 15 minutes followed by at least one wash in 0.2X SCC, 0.1% SDS at room temperature for at least 3-5 minutes.

A further aspect is the use of the isolated polynucleotide sequences of the invention in performing a genetic engineering event (such as transposon insertion, or site specific mutation or deletion, but preferably a homologous recombination event) within 1000 bp upstream of a Gram-negative bacterial chromosomal gene in order to either increase or decrease expression of the gene. Preferably the strain in which the recombination event is to take place is the same as the strain from which the upstream sequences of the invention were obtained. However, the meningococcus A, B, C, Y and W and gonococcus genomes are sufficiently similar that upstream sequence from any of these strains may be suitable for designing vectors for performing such events in the other strains. This is may also be the case for *Haemophilus influenzae* and non-typeable *Haemophilus influenzae*.

## EXAMPLES

The examples below are carried out using standard techniques, which are well known and routine to those of skill in the art, except where otherwise described in detail. The  
5 examples are illustrative, but do not limit the invention.

### Example 1: Construction of a *Neisseria meningitidis* serogroup B strain lacking capsular polysaccharides.

10 The plasmid pMF121 (Frosch et al., 1990) has been used to construct a *Neisseria meningitidis* B strain lacking the capsular polysaccharide. This plasmid contains the flanking regions of the gene locus coding for the biosynthesis pathway of the group B polysaccharide (B PS), and the erythromycin resistance gene. Deletion of the B PS resulted in loss of expression of the group B capsular polysaccharide as well as a  
15 deletion in the active copy of *galE* leading to the synthesis of galactose deficient LPS.

#### Strain transformation:

*Neisseria meningitidis* B H44/76 strain (B:15:P1.7, 16;Los 3,7,9) was selected for transformation. After an overnight CO<sub>2</sub> incubation on MH plate (without  
20 erythromycin), cells were collected in liquid MH containing 10 mM MgCl<sub>2</sub> (2 ml were used per MH plate) and diluted up to an OD of 0.1 (550 nm). To this 2 ml solution, 4 µl of the plasmid pMF121 stock solution (0.5 µg/ml) were added for a 6 hours incubation period at 37°C (with shaking). A control group was done with the same amount of *Neisseria meningitidis* B bacteria, but without addition of plasmid.  
25 After the incubation period, 100 µl of culture, as such, at 1/10, 1/100 and 1/1000 dilutions, were put in MH plates containing 5, 10, 20, 40 or 80 µg erythromycin /ml before incubation for 48 hours at 37°C.

#### Colony blotting:

30 After plate incubation, 20 colonies were grown and selected from the 10 and 20 µg erythromycin/ml MH plates, while there was no colony growth in the control group without plasmid transformation. The H44/76 wild type strain was unable to grow in

the selected erythromycin plates (10 to 80 µg erythromycin/ml). The day after, all the visible colonies were placed on new MH plates without erythromycin in order to let them grow. Afterwards, they were transferred onto nitrocellulose sheets (colony blotting) for presence of B polysaccharide. Briefly, colonies were blotted onto a nitrocellulose sheet and rinsed directly in PBS-0.05 % Tween 20 before cell inactivation for 1 hour at 56°C in PBS-0.05% Tween 20 (diluant buffer). Afterwards, the membrane was overlaid for one hour in the diluant buffer at room temperature (RT). Then, sheets were washed again for three times 5 minutes in the diluant buffer before incubation with the anti-B PS 735 Mab (Boehringer) diluted at 1/3000 in the diluant buffer for 2 hours at RT. After a new washing step (3 times 5 minutes), the monoclonal antibody was detected with a biotinylated anti-mouse Ig from Amersham (RPN 1001) diluted 500 times in the diluant buffer (one hour at RT) before the next washing step (as described above). Afterwards, sheets were incubated for one hour at RT with a solution of streptavidin-peroxidase complex diluted 1/1000 in the diluant buffer. After the last three washing steps using the same method, nitrocellulose sheets were incubated for 15 min in the dark using the revelation solution (30 mg of 4-chloro-1-naphtol solution in 10 ml methanol plus 40 ml PBS and 30 mcl of H<sub>2</sub>O<sub>2</sub> 37% from Merck). The reaction was stopped with a distilled water-washing step.

#### 20 Whole cell Elisas:

Whole cell Elisas were also done using the two transformed colonies ("D" and "R") and the wild type strain (H44/76) as coated bacteria (20 µg protein/ml), and a set of different monoclonal antibodies used to characterize *Neisseria meningitidis* strains. The following Mabs were tested: anti-B PS (735 from Dr Frosch), and the other Mabs from NIBSC: anti-B PS (Ref 95/750) anti-P1.7 (A-PorA, Ref 4025), anti-P1.16 (A-PorA, Ref 95/720), anti-Los 3,7,9 (A-LPS, Ref 4047), anti-Los 8 (A-LPS, Ref 4048), and anti-P1.2 (A-PorA Ref 95/696).

Microtiter plates (Maxisorp, Nunc) were coated with 100 µl of the recombinant meningococcal B cells solution overnight (ON) at 37°C at around 20 µg/ml in PBS. Afterwards, plates are washed three times with 300 µl of 150 mM NaCl - 0.05 % Tween 20, and were overlaid with 100 µl of PBS-0.3 % Casein and incubated for 30 min at room temperature with shaking. Plates were washed again



using the same procedure before incubation with antibodies. Monoclonal antibodies (100 µl) were used at different dilutions (as shown in Figure 2) in PBS-0.3 % Casein 0.05 % Tween 20 and put onto the microplates before incubation at room temperature for 30 min with shaking, before the next identical washing step. 100 µl of the anti-  
5 mouse Ig (from rabbit, Dakopatts E0413) conjugated to biotin and diluted at 1/2000 in PBS-0.3 % Casein - 0.05 % Tween 20 were added to the wells to detect bound monoclonal antibodies. After the washing step (as before), plates were incubated with a streptavidin-peroxidase complex solution (100 µl of the Amersham RPN 1051) diluted at 1/4000 in the same working solution for 30 min at room temperature under  
10 shaking conditions. After this incubation and the last washing step, plates are incubated with 100 µl of the chromogen solution (4 mg orthophenylenediamine (OPD) in 10 ml 0.1 M citrate buffer pH4.5 with 5 µl H<sub>2</sub>O<sub>2</sub>) for 15 min in the dark. Plates are then read at 490/620 nm using a spectrophotometer.

#### 15 Results:

Figure 1 shows that from the 20 isolated colonies, which were able to growth on the selected medium with erythromycin, only two (the "D" and the "R") colonies were shown negative for presence of B polysaccharide. Among the others, 16 were clearly positive for B PS and still resistant to erythromycin. This indicated that they  
20 integrated the plasmid into their genome, but in the wrong orientation, and keeping intact the B PS and LPS gene (no double crossing-over). Positive and negative controls were also tested on the plates, and showed that the H44/76 wild type NmB strain was clearly positive for the B polysaccharide, while meningococcus A (A1) and meningococcus C (C11) strains were clearly negative with this anti-B PS 735 Mab.  
25 These results indicate that around 10 % of the selected colonies correctly integrated the plasmid in their genome by making a double crossing-over, while the other strains/colonies were obtained after a simple crossing-over, keeping the B PS and LPS genes intact and expressed.

Using whole cell Elisa, results (Figure 2 and the Table below) clearly indicate  
30 that the two "D" and "R" transformants (derived from D and R colonies) can not be recognized anymore by the anti-B PS Mabs (735 and 95/750), nor by the anti-Los 3,7,9 and anti-Los 8 Mabs. However, when using specific anti-PorA Mabs, there is a

clear reaction with the anti-P1.7 and anti-P1.16 Mabs on the cells, as also observed in the wild-type strain. No reaction was observed with a non-specific anti-PorA Mab (anti-P1.2 mab). These results confirm that the PorA protein, and specifically P1.7 and P1.16 epitopes are still present after transformation, while B polysaccharide and  
 5 Los 3,7,9 and Los 8 epitopes (LPS) were not.

Table : Specificities of the monoclonal antibodies tested

Mabs Tested	Directed against	Result
Anti-B PS 735	B polysaccharide	++ on the wild type strain (-) on the "D" and "R" mutants
Anti-B PS 95/750 from NIBSC	B PS	++ on the wild type strain (-) on the "D" and "R" mutants
Anti-P1.7 (NIBSC)	Loop 1 of Porin A	++ on all wild type and mutants strains
Anti-P1.16 (NIBSC)	Loop 4 of Porin A	++ on all wild type and mutants strains
Anti-Los 3,7,9	LPS	++ on the wild type strain (-) on the "D" and "R" mutants
Anti-Los 8 (NIBSC)	LPS	+/- on the wild type strain (-) on the "D" and "R" mutants
Anti-P1.2 (NIBSC)	Anti-Porin A Sero-subtype 1.2	(-) on all wild type and mutants strains

10 **Example 2: Construction of versatile gene delivery vectors (the pCMK series) targeting integration in the *porA* locus of *Neisseria meningitidis*.**

A plasmid allowing homologous recombination and stable integration of foreign DNA in the *porA* locus of *Neisseria meningitidis* was constructed. This  
 15 delivery vector (genes, operons and/or expression cassettes) is useful for constructing *Neisseria meningitidis* strains producing recombinant, improved blebs. Typically, such a vector contains at least: (1) a plasmid backbone replicative in *E. coli* but not in *Neisseria meningitidis* (a suicide plasmid), (2) at least one, but preferably two regions

of homology for targeting the integration in a chromosomal locus such as *porA*, (3) Efficient transcriptional (promoter, regulatory region and terminator) and translational (optimised ribosome binding site and initiation codon) signals functional in *Neisseria meningitidis*, (4) a multiple cloning site and (5) selectable gene(s) allowing the  
 5 maintenance of the plasmid in *E. coli* and the selection of integrants in *Neisseria meningitidis*. Additional elements include, for example, uptake sequences to facilitate the entry of foreign DNA in *Neisseria meningitidis*, and counter selectable markers such as *sacB*, *rpsL*, *gltS* to enhance the frequency of double cross-over events.

A schematic drawing of the vector constructed in this example and designated  
 10 pCMK is represented in Figure 3. Its corresponding complete nucleotide sequence is shown in SEQ. ID NO:1. pCMK derives from a pSL1180 backbone (PharmaciaBiotech, Sweeden), a high copy-number plasmid replicative in *E. coli*, harbouring the *bla* gene (and thereby conferring resistance to ampicillin). In addition to this, pCMK functionally contains two *porA* flanking regions (*porA5'* and *porA3'*  
 15 containing a transcription terminator) necessary for homologous recombination, a selectable marker conferring resistance to kanamycin, two uptake sequences, a *porA/lacO* chimeric promoter repressed in the *E.coli* host expressing *lacIq* but transcriptionally active in *Neisseria meningitidis*, and a multiple cloning site (5 sites present: *NdeI*, *KpnI*, *NheI*, *PstI* and *SphI*) necessary for the insertion of foreign  
 20 DNA in pCMK.

pCMK was constructed as follows. The *porA5'* and *porA3'* recombinogenic regions, the *porA/lacO* promoter were PCR amplified using the oligonucleotides listed in the table below, cloned in pTOPO and sequenced. These DNA fragments were successively excised from pTOPO and recloned in pSL1180. The kanamycin  
 25 resistance cassette was excised from pUC4K (PharmaciaBiotech, Sweeden) and was introduced between the *porA5'* flanking region and the *porA/lacO* promoter region.

***Table: Oligonucleotides used in this work***

Oligonucleotides	Sequence	Remark(s)
PorA5' Fwd	5'-CCC AAG CTT GCC GTC TGA ATA CAT CCC GTC ATT CCT CA-3'	<i>Hind</i> III cloning site Uptake sequence ( _ )
PorA5' Rev	5'-CGA TGC TCG CGA CTC CAG AGA CCT CGT GCG GGC C-3'	<i>Nru</i> I cloning site
PorA3' Fwd	5'-GGA AGA TCT GAT TAA ATA GGC GAA AAT ACC AGC TAC GA-3'	<i>Bgl</i> II cloning site Stop codons ( _ )
PorA3' Rev	5'-GCC GAA TTC TTC AGA CGG C GC AGC AGG AAT TTA TCG G-3'	<i>Eco</i> RI cloning site Uptake sequence ( _ )
PoLa Rev1	5'- GAA TTG TTA TCC GCT CAC AAT TCC GGG CAA ACA CCC GAT AC-3'	
PoLa Rev2	5'-GAA TTC CAT ATG ATC GGC TTC CTT TTG TAA ATT TGA TAA AAA CCT AAA AAC ATC GAA TTG TTA TCC GCT C-3'	<i>Nde</i> I cloning site
PorAlacO Fwd	5'-AAG CTC TGC AGG AGG TCT GCG CTT GAA TTG-3'	<i>Pst</i> I cloning site
PorAlacO Rev	5'-CTT AAG GCA TAT GGG CTT CCT TTT GTA A- 3'	<i>Nde</i> I cloning site
PPA1	5'- GCG GCC GTT GCC GAT GTC AGC C-3'	
PPA2	5'-GGC ATA GCT GAT GCG TGG AAC TGC-3'	
N-full-01:	5'-GGG AAT TCC ATA TGA AAA AAG CAC TTG CCA CAC-3'	<i>Nde</i> I cloning site
Nde-NspA-3:	5'- GGA ATT CCA TAT GTC AGA ATT TGA CGC GCA C -3'	<i>Nde</i> I cloning site
PNS1	5'- CCG CGA ATT CGG AAC CGA ACA CGC CGT TCG-3'	<i>Eco</i> RI cloning site
PNS1	5'- CGT CTA GAC GTA GCG GTA TCC GGC TGC -3'	<i>Xba</i> I cloning site
PromD15-51X	5'- GGG CGA ATT CGC GGC CGC CGT CAA CGG CAC ACC CGT TG-3'	<i>Eco</i> RI and <i>Not</i> I cloning sites
PromD15-S2	5'- GCT CTA GAG CGG AAT GCG GTT TCA GAC G- 3'	<i>Xba</i> I cloning site
PNS4	5'- AGC TTT ATT TAA ATC CTT AAT TAA CGC GTC CGG AAA ATA TGC TTA TC_34	<i>Swa</i> I and <i>Pac</i> I cloning sites
PNS5	5'- AGC TTT GTT TAA ACC CTG TTC CGC TGC TTC GGC-3'	<i>Pme</i> I cloning site
D15-S4	5'- GTC CGC ATT TAA ATC CTT AAT TAA GCA GCC GGA CAG GGC GTG G-3'	<i>Swa</i> I and <i>Pac</i> I cloning sites
D15-S5	5'- AGC TTT GTT TAA AGG ATC AGG GTG TGG TCG GGC-3'	<i>Pme</i> I cloning site

**Example 3: Construction of a *Neisseria meningitidis* serogroup B strain lacking both capsular polysaccharides and the major immunodominant antigen PorA.**

Modulating the antigenic content of outer membrane blebs may be  
5 advantageous in improving their safety and efficacy in their use in vaccines, or  
diagnostic or therapeutic uses. Components such as the *Neisseria meningitidis*  
serogroup B capsular polysaccharides should be removed to exclude the risk of  
inducing autoimmunity (see example 1). Similarly, it is beneficial to suppress the  
immunodominance of major outer-membrane antigens such as PorA, which induce  
10 strain-specific bactericidal antibodies but fail to confer cross-protection. To illustrate  
such an approach, we used the pCMK(+) vector to construct a *Neisseria meningitidis*  
serogroup B strain lacking both capsular polysaccharides and the immunodominant  
PorA outer membrane protein antigen. For this purpose, a deletion of the *porA* gene  
was introduced in the H44/76 *cps*- strain, described in example 1 by means of  
15 homologous recombination.

The H44/76 *cps*- strain was prepared competent and transformed with two 2µg  
of supercoiled pCMK(+) plasmid DNA as described previously. Aliquot fractions of  
the transformation mixture (100µl) were plated on Mueller-Hinton plates  
supplemented with Kanamycin (200µg/ml) and incubated at 37°C for 24 to 48 hours.  
20 Kanamycin-resistant colonies were selected, restreaked on MH-Kn and grown for an  
additional 24 hours at 37°C. At that stage half of the bacterial culture was used to  
prepare glycerol stocks (15 % vol./vol.) and was kept frozen at -70°C. Another  
fraction (estimated to be 10<sup>8</sup> bacteria) was resuspended in 15 µl of distilled water,  
boiled ten minutes and used as a template for PCR screening. Two *porA* internal  
25 primers named , PPA1 and PPA2, were synthesized and used to perform PCR  
amplification on boiled bacterial lysates in the conditions described by the supplier  
(HiFi DNA polymerase, Boehringer Mannheim, GmbH). The thermal cycling used  
was the following: 25 times (94°C 1min., 52°C 1min., 72°C 3min.) and 1 time (72°C  
10min., 4°C up to recovery). Since a double crossing-over between pCMK DNA and  
30 the chromosomal *porA* locus deletes the region required for #1 and #2 annealing,  
clones lacking a 1170bp PCR amplification fragment were selected as *porA* deletion  
mutants. These PCR results were further confirmed by analyzing in parallel, the

presence of PorA in the corresponding bacterial protein extracts. For that purpose, another aliquot of bacteria (estimated to be  $5 \cdot 10^8$  bacteria) was re-suspended in 50  $\mu$ l of PAGE-SDS buffer (SDS 5%, Glycerol 30%, Beta-mercaptoethanol 15%, Bromophenol blue 0.3mg/ml, Tris-HCl 250 mM pH6.8), boiled (100°C) frozen (-20°C) / boiled (100°C) three times and was separated by PAGE-SDS electrophoresis on a 12.5 % gel. Gels were then stained by Coomassie Brilliant blue R250 or transferred to a nitrocellulose membrane and probed with an anti-PorA monoclonal antibody as described in Maniatis *et al.* As represented in Figure 4, both Coomassie and immunoblot staining confirmed that *porA* PCR negative clones do not produce detectable levels of PorA. This result confirm that the pCMK vector is functional and can be used successfully to target DNA insertion in the *porA* gene, abolishing concomitantly the production of the PorA outer membrane protein antigen.

**Example 4: Up-regulation of the NspA outer membrane protein production in blebs derived from a recombinant *Neisseria meningitidis* serogroup B strain lacking functional *porA* and *cps* genes.**

Enriching bleb vesicles with protective antigens is advantageous for improving the efficiency and the coverage of outer membrane protein-based vaccines. In that context, recombinant *Neisseria meningitidis* strains lacking functional *cps* and *porA* genes were engineered so that the expressions level of the outer-membrane protein NspA was up-regulated. For that purpose, the gene coding for NspA was PCR amplified using the N01-full-*NdeI* and *NdeI*-3' oligonucleotide primers (see table in example 2). The conditions used for PCR amplification were those described by the supplier (HiFi DNA polymerase, Boehringer Mannheim, GmbH). Thermal cycling done was the following: 25 times (94°C 1min., 52°C 1min., 72°C 3min.) and 1 time (72°C 10min., 4°C up to recovery). The corresponding amplicon was digested with *NdeI* and inserted in the *NdeI* restriction site of the pCMK(+) delivery vector. Insert orientation was checked and recombinant plasmids, designed pCMK(+)-NspA, were purified at a large scale using the QIAGEN maxiprep kit and 2  $\mu$ g of this material was used to transform a *Neisseria meningitidis* serogroup B strain lacking functional *cps*

genes (strain described in example 1). Integration resulting from a double crossing-over between the pCMK(+)-NspA vector and the chromosomal *porA* locus were selected using a combination of PCR and Western blot screening procedures presented in example 3.

5 Bacteria (corresponding to about  $5 \cdot 10^8$  bacteria) were re-suspended in 50  $\mu$ l of PAGE-SDS buffer, frozen(-20°C) / boiled (100°C) three times and then were separated by PAGE-SDS electrophoresis on a 12.5 % gel. Gels were then stained by Coomassie Brilliant blue R250 or transferred to a nitrocellulose membrane and probed with an anti-NspA polyclonal serum. Both Coomassie (data not shown) and  
10 immunoblot staining (see figure 4) confirmed that *porA* PCR negative clones do not produce detectable levels of PorA. The expression of NspA was examined in Whole-cell bacterial lysates (WCBL) or outer-membrane bleb preparations derived from NmB [*cps*-, *porA*-] or NmB [*cps*-, *porA*-, *Nspa*+]. Although no difference was observable by Coomassie staining, immunoblotting with the anti-NspA polyclonal  
15 serum detected a 3-5 fold increased in the expression of NspA (with respect to the endogenous NspA level), both in WCBL and outer-membrane bleb preparations (see figure 5). This result confirm that the pCMK(+)-NspA vector is functional and can be used successfully to up-regulate the expression of outer membrane proteins such as NspA, abolishing concomitantly the production of the PorA outer membrane protein  
20 antigen.

**Example 5: Up-regulation of the D15/Omp85 outer membrane protein antigen in blebs derived from a recombinant *Neisseria meningitidis* serogroup B strain lacking functional *cps* genes but expressing PorA.**

25 Certain geographically isolated human populations (such as Cuba) are infected by a limited number of *Neisseria meningitidis* isolates belonging largely to one or few outer membrane protein serotypes. Since PorA is a major outer-membrane protein antigen inducing protective and strain-specific bactericidal antibodies, it is then  
30 possible to confer vaccine protection using a limited number of *porA* serotypes in a vaccine. In such a context, the presence of PorA in outer membrane vesicles may be advantageous, strengthening the vaccine efficacy of such recombinant improved

blebs. Such PorA containing vaccines, however, can be improved still further by increasing the level of other cross-reactive OMPs such as omp85/D15.

In the following example, the pCMK(+) vector was used to up-regulate the expression of the Omp85/D15 outer membrane protein antigen in a strain lacking functional *cps* genes but expressing *porA*. For that purpose, the gene coding for Omp85/D15 was PCR amplified using the D15-*NdeI* and D15-*NotI* oligonucleotide primers. The conditions used for PCR amplification were those described by the supplier (HiFi DNA polymerase, Boehringer Mannheim, GmbH). Thermal cycling done was the following: 25 times (94°C 1min., 52°C 1min., 72°C 3min.) and 1 time (72°C 10min., 4°C up to recovery). The corresponding amplicon was inserted in the pTOPO cloning vector according to the manufacturer's specifications and confirmatory sequencing was performed. This Omp85/D15 DNA fragment was excised from pTOPO by restriction hydrolysis using *NdeI/NsiI* and subsequently cloned in the corresponding restriction sites of the pCMK(+) delivery vector. Recombinant plasmids, designed pCMK(+)-D15 were purified on a large scale using the QIAGEN maxiprep kit and 2 µg of this material was used to transform a *Neisseria meningitidis* serogroup B strain lacking functional *cps* genes (strain described in example 1). In order to preserve the expression of *porA*, integration resulting from a single crossing-over (either in Omp85/D15 or in *porA*) were selected by a combination of PCR and Western blot screening procedures. Kanamycin resistant clones testing positive by *porA*-specific PCR and western blot were stored at -70°C as glycerol stocks and used for further studies.

Bacteria (corresponding to about  $5.10^8$  bacteria) were re-suspended in 50 µl of PAGE-SDS buffer, frozen(-20°C) / boiled (100°C) three times and then were separated by PAGE-SDS electrophoresis on a 12.5 % gel. Gels were then stained by Coomassie Brilliant blue R250 or transferred to a nitrocellulose membrane and probed with an anti-*porA* monoclonal antibody. As represented in Figure 6, both Coomassie and immunoblot staining confirmed that *porA* PCR positive clones produce PorA.

The expression of D15 was examined using outer-membrane bleb preparations derived from NmB [*cps*-, *porA*-] or NmB [*cps*-, *porA*+, D15+]. Coomassie detected a significant increase in the expression of D15 (with respect to the endogenous D15 level), preparations (see Figure 6). This result confirmed that the pCMK(+)-D15



vector is functional and can be used successfully to up-regulate the expression of outer membrane proteins such as D15, without abolishing the production of the major PorA outer membrane protein antigen.

5 **Example 6: Construction of versatile promoter delivery vectors**

Rational: The rational of this approach is represented in Figure 7 and can be summarized in 7 essential steps. Some of these steps are illustrated below with the construction of Vector for up-regulating the expression of NspA and D15/Omp85.

10

Vector for up-regulating the expression of the NspA gene.

**Step 1.** A DNA region (997bp) located upstream from the NspA coding gene was discovered (SEQ. ID NO:2) in the private Incyte PathoSeq data base containing unfinished genomic DNA sequences of the *Neisseria meningitidis* strain ATCC  
15 13090. Two oligonucleotide primers referred to as PNS1 and PNS2 (see table in example 2) were designed using this sequence and synthesized. These primers were used for PCR amplification using genomic DNA extracted from the H44/76 strain.  
**Step 2.** The corresponding amplicons were cleaned-up using the Wizard PCR kit (Promega, USA) and submitted to digestion with the *EcoRI/XbaI* restriction enzymes  
20 for 24 hours using the conditions described by the supplier (Boehringer Mannheim, Germany). The corresponding DNA fragments were gel purified and inserted in the corresponding sites of the pUC18 cloning vector. **Step 3.** Recombinant plasmids were prepared on a large scale and an aliquot fraction was used as a template for inverse PCR amplification. Inverse PCR was performed using the PNS4 and PNS5  
25 oligonucleotides using the following thermal cycling conditions: 25 times (94°C 1min., 50°C 1min., 72°C 3min.) and 1 time (72°C 10min., 4°C up to recovery). Linearized pUC 18 vectors harbouring a deletion in the NspA upstream region insert were obtained.

30 Vector for up-regulating the expression of the D15/omp85 gene.

**Step 1.** A DNA region (1000 bp) located upstream from the D15/omp85 coding gene was discovered (SEQ. ID NO:3) in the private Incyte PathoSeq database containing

unfinished genomic DNA sequences of the *Neisseria meningitidis* strain ATCC 13090. Two oligonucleotide primers referred to as PromD15-51X and PromD15-S2 (see table in example 2) were designed using this sequence and synthesized. These primers were used for PCR amplification using genomic DNA extracted from the H44/76 strain. **Step 2.** The corresponding amplicons were cleaned-up using the Wizard PCR kit (Promega, USA) and submitted to digestion with the *EcoRI/XbaI* restriction enzymes for 24 hours in the conditions described by the supplier (Boehringer Mannheim, Germany). The corresponding DNA fragments were gel purified and inserted in the corresponding sites of the pUC18 cloning vector. **Step 3.** Recombinant plasmids were prepared on a large scale and an aliquot fraction was used as a template for inverse PCR amplification. Inverse PCR was performed using the D15-S4 and D15-S5 oligonucleotides using the following thermal cycling conditions: 25 times (94°C 1min., 50°C 1min., 72°C 3min.) and 1 time (72°C 10min., 4°C up to recovery). Linearized pUC 18 vectors harbouring a deletion in the D15/omp85 upstream region insert were obtained.

**Example 7: Fermentation processes for producing recombinant blebs .**

The examples listed below describe methods for producing recombinant blebs lacking either capsular polysaccharides or capsular polysaccharides and PorA. Such a procedure may be used for a wide range of *Neisseria meningitidis* recombinant strains and may be adapted over an extended scale range.

Culture media: *Neisseria meningitidis* serogroup B strains were propagated in solid (FNE 004 AA, FNE 010 AA) or liquid (FNE 008 AA) culture media. These new media for growing meningococcus are advantageously free of animal products, and are considered a further aspect of the invention.

Components	FNE 004 AA	FNE 008 AA	FNE 010 AA
Agar	18 g/L	-	18 g/L
NaCl	6 g/L	6 g/L	6 g/L
Na-Glutamate	-	1.52 g/L	-
NaH <sub>2</sub> PO <sub>4</sub> ·2H <sub>2</sub> O	2.2 g/L	2.2 g/L	2.2 g/L
KCl	0.09 g/L	0.09 g/L	0.09 g/L
NH <sub>4</sub> Cl	1.25 g/L	1.25 g/L	1.25 g/L
Glucose	5 g/L	20 g/L	5 g/L
Yeast Extract UF	-	2.5 g/L	-
Soy Pepton	5 g/L	30 g/L	5 g/L
CaCl <sub>2</sub> ·2H <sub>2</sub> O	0.015 g/L	-	0.015 g/L
MgSO <sub>4</sub> ·7H <sub>2</sub> O	0.6 g/L	0.6 g/L	0.6 g/L
Erythromycine :	0.015 g/L	-	-
Kanamycine	-	-	0.2 g/L

5 Flask cultivation of *Neisseria meningitidis* serogroup B cps- recombinant blebs: This was performed in two steps comprising preculture on solid medium followed by liquid cultivation. **Solid pre-culture** A vial of seed was removed from freezer (-80°C), thawed to room temperature and 0.1 mL was streaked into a Petri dish containing 15 mL of FNE004AA (see above). The Petri dish was incubated at 37°C for 18 ± 2 hours. The surface growth was resuspended in 8 mL of FNE008AA (see above) supplemented with 15 mg/L of erythromycin. **Flask culture.** 2 mL of resuspended solid pre-culture were added to a 2 litre flask containing 400 mL of FNE008AA supplemented with 15 mg/L of erythromycin. The flask was placed on a shaking table (200 rpm) and incubated at 37°C for 16 ± 2 hours. The cells were separated from the culture broth by centrifugation at 5000g at 4°C for 15 minutes.

15

20 Batch mode cultivation of *Neisseria meningitidis* serogroup B cps- recombinant blebs: This was performed in three steps comprising preculture on solid medium, liquid cultivation and batch mode cultivation. **Solid pre-culture.** A vial of seed was removed from freezer (-80°C), thawed to room temperature and 0.1 mL was streaked into a Petri dish containing 15 mL of FNE004AA (see above). The Petri dish was

incubated at 37°C for 18 ± 2 hours. The surface growth was resuspended in 8 mL of FNE008AA (see above) supplemented with 15 mg/L of erythromycin. **Liquid pre-culture.** 2 mL of resuspended solid pre-culture were added to one 2 liters flask containing 400 mL of FNE008AA supplemented with 15 mg/L of erythromycin. The flask was placed on a shaking table (200 rpm) and incubated at 37°C for 16 ± 2 hours. The content of the flask was used to inoculate the 20 liters fermenter. **Batch mode culture in fermenter.** The inoculum (400 mL) was added to a pre-sterilized 20 liters (total volume) fermenter containing 10 L of FNE008AA supplemented with 15 mg/L of erythromycin. The pH was adjusted to and maintained at 7.0 by the automated addition of NaOH (25% w/v) and H<sub>3</sub>PO<sub>4</sub> (25% v/v). The temperature was regulated at 37°C. The aeration rate was maintained at 20 L of air / min and the dissolved oxygen concentration was maintained at 20% of saturation by the agitation speed control. The overpressure in the fermenter was maintained at 300 g/cm<sup>2</sup>. After 9 ± 1 hours, the culture was in stationary phase. The cells were separated from the culture broth by centrifugation at 5000g at 4°C for 15 minutes.

Flask cultivation of *Neisseria meningitidis* serogroup B cps-, PorA- recombinant blebs: This was performed in two steps comprising preculture on solid medium followed by liquid cultivation. **Solid pre-culture.** A vial of seed was removed from freezer (-80°C), thawed to room temperature and 0.1 mL was streaked into a Petri dish containing 15 mL of FNE010AA (see above). The Petri dish was incubated at 37°C for 18 ± 2 hours. The surface growth was resuspended in 8 mL of FNE008AA (see above) supplemented with 200 mg/L of kanamycin. **Flask culture.** 2 mL of resuspended solid pre-culture were added to a 2 litre flask containing 400 mL of FNE008AA supplemented with 200 mg/L of kanamycin. The flask was placed on a shaking table (200 rpm) and incubated at 37°C for 16 ± 2 hours. The cells were separated from the culture broth by centrifugation at 5000g at 4°C for 15 minutes.

Example 8: Isolation and purification of blebs from meningococci devoid of capsular polysaccharide

5 Recombinant blebs were purified as described below. The cell paste (42gr) was suspended in 211 ml of 0.1M Tris-Cl buffer pH 8.6 containing 10 mM EDTA and 0.5% Sodium Deoxycholate (DOC). The ratio of buffer to biomass was 5/1 (V/W). The biomass was extracted by magnetic stirring for 30 minutes at room temperature. Total extract was then centrifuged at 20,000g for 30 minutes at 4°C (13,000 rpm in a  
10 JA-20 rotor, Beckman J2-HS centrifuge). The pellet was discarded. The supernatant was ultracentrifuged at 125,000g for 2 hours at 4°C (40,000 rpm in a 50.2Ti rotor, Beckman L8-70M ultracentrifuge) in order to concentrate vesicles. The supernatant was discarded. The pellet was gently suspended in 25 ml of 50 mM Tris-Cl buffer pH 8.6 containing 2 mM EDTA, 1.2% DOC and 20% sucrose. After a second  
15 ultracentrifugation step at 125,000g for 2 hours at 4°C, vesicles were gently suspended in 44 ml of 3% sucrose and stored at 4°C. All solutions used for bleb extraction and purification contained 0.01% thiomersalate. As illustrated in Figure 8, this procedure yields protein preparations highly enriched in outer-membrane proteins such as PorA and PorB.

20

Example 9: Identification of bacterial promoters suitable for up-regulation antigens-coding genes

The use of strong bacterial promoter elements is essential to obtain up-regulation of genes coding for outer membrane proteins. In that context, we have  
25 shown previously that up-regulating the *Neisseria meningitidis* *nspA*, *hsf*, and *omp85* genes using the *porA* promoter has allowed us to isolate recombinant blebs enriched in the corresponding NspA, Hsf and Omp85 proteins. Alternatives to the *porA* promoter may be useful to obtain different levels of up-regulation, to overcome potential *porA* phase variation and/or to achieve conditional gene expression (iron-  
30 regulated promoters). Here we describe a method allowing the identification of a precise transcriptional start site of strong promoter elements likely to confer high level of expression in bacteria. Since promoter regulatory elements are classically

encompassed within 200 bp upstream and 50bp downstream from the +1 site (Collado-Vides J, Magasanik B, Gralla JD, 1991, *Microbiol Rev* 55(3):371-94), the result of such an experiment allows us to identify DNA fragments of about 250 bp carrying strong promoter activities. Major outer membrane proteins such as *Neisseria meningitidis* PorA, PorB & Rmp, *Haemophilus influenzae* P1, P2, P5 & P6, *Moraxella catarrhalis* OmpCD, OmpE, as well as some cytoplasmic and/or iron regulated proteins of these bacteria possess strong promoter elements. As a validation of this general methodology, we mapped the transcriptional start site of the strong *Neisseria meningitidis* *porA* and *porB* promoters using rapid amplification of cDNA elements (5' RACE).

The principles of 5' RACE are the following: 1) Total RNA extraction using QIAGEN "RNeasy" Kit. Genomic DNA removing by DNase treatment followed by QIAGEN purification; 2) mRNA reverse transcription with a *porA* specific 3' end primer (named *porA3*). Expected cDNA size: 307 nt. RNA removing by alkaline hydrolysis; 3) Ligation of a single-stranded DNA oligo anchor (named DT88) to the 3' end of the cDNA using T4 RNA ligase. Expected product size: 335 nt. Amplification of the anchor-ligated cDNA using a combination of hemi-nested PCR; 4) PCR amplification of the anchor-ligated cDNA using a complementary-sequence anchor primer as the 5' end primer (named DT89) and a 3'end primer (named p1-2) which is internal to the 3'end RT primer *porA3*. Expected product size: 292 bp; 5) PCR amplification of previous PCR products using DT89 as 5'end primer and p1-1 as 3'end primer (internal to p1-2). Expected product size: 211bp; and 6) Sequencing with p1-1 primer (expected products size can be calculated because *porA* transcription start site is known: 59 nt before the "ATG" translation start site).

### Experimental procedure

Total RNA was extracted from approximately  $10^9$  cells of *Neisseria meningitidis* serogroup B *cps- porA+* strain. Extraction of 1 ml of a liquid culture at appropriate optical density ( $OD_{600} = 1$ ) was performed by the QIAGEN "RNAeasy" kit according to the manufacturer's instructions. Chromosomal DNA was removed by addition of 10U of RNase-free DNase (Roche Diagnostics, Mannheim, Germany) to the 30  $\mu$ l of eluted RNA and was

incubated at 37°C for 15 min. The DNA-free RNA was purified with the same QIAGEN kit according to instructions.

Reverse transcription reactions were performed using primer porA3 and 200U of SUPERScript II reverse transcriptase (Life Technologies). The RT reactions were performed in a 50µl volume containing: 5µl of 2mM dNTP, 20 pmol of porA3 primer, 5µl of 10X SUPERScript II buffer, 9µl of 25mM MgCl<sub>2</sub>, 4µl of 0.1M DTT, 40U of recombinant ribonuclease inhibitor and 1 µg of total RNA. The porA3 primer was annealed stepwise (70°C for 2 min, 65°C for 1 min, 60°C for 1 min, 55°C for 1 min, 50°C for 1 min, and 45°C for 1 min) before the SUPERScript II was added. The RT reaction was performed at 42°C for 30 min, followed by 5 cycles (50°C for 1 min, 53°C for 1 min and 56°C for 1 min) to destabilize RNA secondary structure. Two parallel reactions were performed with the reverse transcriptase omitted from one reaction as negative control.

The RNA was removed by alkaline hydrolysis cleavage with the addition of 1 µl of 0.5M EDTA followed by 12.5 µl of 0.2 M NaOH before incubation at 68°C for 5 min. The reactions were neutralized by adding 12.5 µl of 1 M Tris-HCl (pH7.4) and precipitated by the addition of 20 µg of glycogen (Roche Molecular Biochemicals, Mannheim, Germany), 5 µl of 3 M sodium acetate and 60 µl of isopropanol. Both samples were resuspended in 20 µl of 10:1 TE (10 mM Tris-HCl, pH 7.4; 1 mM EDTA, pH8).

T4 RNA ligase was used to anchor a 5'-phosphorylated, 3'-end ddCTP-blocked anchor oligonucleotide DT88 (see table below). Two parallel ligations were performed overnight at room temperature with each containing: 1.3 µl of 10X RNA ligase buffer (Roche Molecular Biochemicals), 0.4 µM DT88, 10 µl of either cDNA or RT control sample and 3 U of T4 RNA ligase. As negative controls, a second set of ligation reactions was performed, omitting the T4 RNA ligase. The resulting ligation-reaction mixtures were used directly without purification in the subsequent PCR.

The anchor-ligated cDNA was amplified using a combination of hemi-nested and hot-started PCR approaches to increase specificity and product yield. Four separate first-round PCR were performed on the RT/ligase reaction and controls in a 30 µl volume, each containing: 3 µl of 10X Taq Platinum buffer, 3µl of 25 mM MgCl<sub>2</sub>, 1 µl of 10mM dNTP, 10 pmol of each primers and 1 µl of corresponding RNA ligation reaction. The PCR were hot started by the use of Taq Platinum (Life Technologies) DNA polymerase (2U added). The first ligation-anchored PCR (LA-PCR) was performed using 10 pmol of both the anchor-specific primer DT89 and the transcript-specific primer p1-2 (see table below) which is internal to the 3' end RT primer porA3. The PCR was performed using an initial 95°C for a 5 min step (for DNA polymerase activation) followed by 10 cycles at 95°C for 10 s and 70°C

for 1 min (reducing one degree per cycle), 15 cycles at 95°C for 10 s and 60°C for 1 min. The second hemi-nested LA-PCR was performed under the same conditions using primer DT89 and the p1-2 internal primer, together with 10 pmol of p1-1 (see table below) and 1 µl of first-round PCR. Amplification products were purified using the QIAGEN "QIAquick PCR purification" kit according to manufacturer instructions before submitted to sequencing.

The CEQ™ Dye Terminator Cycle Sequencing kit (Beckman, France) was used to sequence the RACE PCR products using 10 pmol of primer p1-1. Sequencing reactions were performed according to the provided instructions and sequencing products were analyzed by the Ceq2000 DNA Analysis System (Beckman-Coulter).

DT88	5' GAAGAGAAGGTGGAAATGGCGTTTTGGC 3'
DT89	5' CCAAAACGCCATTTCCACCTTCTCTTC 3'
porA3	5' CCAAATCCTCGCTCCCCTTAAAGCC 3'
p1-2	5' CGCTGATTTTCGTCCTGATGCGGC 3'
p1-1	5' GGTCAATTGCGCCTGGATGTTCTCTG 3'

#### **Results for the *Neisseria meningitidis* porA promoter**

The start of transcription for *Neisseria meningitidis* serogroup B (strain H44/76) *porA*-mRNA was mapped 59 bp upstream of the ATG start codon using the described 5'-RACE procedure. This result confirms the mapping performed by primer extension and published by van der Ende *et al* (1995). This result supports that a DNA fragment containing nucleotides -9 to -259 with regard to the *porA* ATG is suitable for driving strong gene expression in *Neisseria meningitidis* and possibly in other bacterial species such as *Haemophilus*, *Moraxella*, *Pseudomonas*.

#### **Results for the *Neisseria meningitidis* porB promoter**

The same experimental strategy has been applied for *Neisseria meningitidis* serogroup B (strain H44/76) *porB* transcription start site mapping. Primers listed in the table below correspond to 3' end RT primer (porB3), transcript-specific primer that is internal to the *porB3* (porB2) and internal to the *porB2* (porB1). *porB3*, *porB2* and *porB1* are respectively located 265 bp, 195 bp and 150 bp downstream the ATG start codon.

porB1	5' GGTAGCGGTTGTAACCTTCAGTAACTT 3'
porB2	5' GTCTTCTTGGCCTTTGAAGCCGATT 3'
porB3	5' GGAGTCAGTACCGGCGATAGATGCT 3'

Using *porB1* and DT89 primers a ~200 bp PCR amplicon was obtained by performing 5' - RACE mapping. Since *porB1* is located 150 bp from the *porB* ATG start



codon, this result supports that the *porB* transcriptional start site is located about 50 bp (+/- 30 bp) upstream of the *porB* ATG.

The exact nucleotide corresponding to transcription initiation is presently being determined by DNA sequencing. The above PCR result supports that a DNA fragment containing nucleotides -1 to -250 with regard to the *porB* ATG start codon is suitable for driving strong gene expression in *Neisseria meningitidis* and possibly in other bacterial species such as *Haemophilus*, *Moraxella*, *Pseudomonas*.

**Example 10: Up-regulation of the *N. meningitidis* serogroup B *Omp85* gene by promoter replacement.**

The aim of the experiment was to replace the endogenous promoter region of the D15/*Omp85* gene by the strong *porA* promoter in order to up-regulate the production of the D15/*Omp85* antigen. For that purpose, a promoter replacement plasmid was constructed using *E. coli* cloning methodologies. A DNA region (1000 bp) located upstream from the *D15/omp85* coding gene was discovered (SEQ ID NO:3) in the private Incyte PathoSeq data base containing unfinished genomic DNA sequences of the *Neisseria meningitidis* strain ATCC 13090. The main steps of this procedure are represented in Figure 9. Briefly, a DNA fragment (1000bp) covering nucleotides -48 to -983 with respect to the *D15/Omp85* gene start codon (ATG) was PCR amplified using oligonucleotides **ProD15-51X** (5'-GGG CGA ATT CGC GGC CGC CGT CAA CGG CAC ACC GTT G-3') and **ProD15-52** (5'-GCT CTA GAG CGG AAT GCG GTT TCA GAC G-3') containing *EcoRI* and *XbaI* restriction sites (underlined) respectively. This fragment was submitted to restriction and inserted in pUC18 plasmid restricted with the same enzymes. The construct obtained was submitted to *in vitro* mutagenesis using the Genome Priming system (using the pGPS2 donor plasmid) commercialized by New England Biolabs (MA, USA). Clones having inserted a mini-transposon (derived from Tn7 and harboring a chloramphenicol resistance gene) were selected. One clone containing a mini-transposon insertion located in the *D15/Omp85* 5' flanking region, 401 bp downstream from the *EcoRI* site was isolated and used for further studies. This plasmid was submitted to circle PCR mutagenesis (Jones & Winistofer (1992), Biotechniques12: 528-534) in order to (i) delete a repeated DNA sequence (Tn7R) generated by the transposition process, (ii) insert meningococcal uptake sequences

required for transformation, and (iii) insert suitable restriction sites allowing cloning of foreign DNA material such as promoters. The circle PCR was performed using the **TnRD15-KpnI/XbaI + US** (5'-CGC CGG TAC CTC TAG AGC CGT CTG AAC CAC TCG TGG ACA ACC C-3') & **TnR03Cam(KpnI)** (5'-CGC CGG TAC CGC CGC TAA CTA TAA CGG TC-3') oligonucleotides containing uptake sequences and suitable restriction sites (*KpnI* and *XbaI*) underlined. The resulting PCR fragment was gel-purified, digested with *Asp718* (isoschizomer of *KpnI*) and ligated to a 184bp DNA fragment containing the *porA* promoter and generated by PCR using the **PorA-01** (5'-CGC CGG TAC CGA GGT CTG CGC TTG AAT TGT G-3') and **PorA02** (5'-CGC CGG TAC CTC TAG ACA TCG GGC AAA CAC CCG-3') oligonucleotides containing *KpnI* restriction sites. Recombinant clones carrying a *porA* promoter inserted in the correct orientation (transcription proceeding in the *EcoRI* to *XbaI* direction) were selected and used to transform a strain of *Neisseria meningitidis* serogroup B lacking capsular polysaccharide (*cps*-) and one of the major outer membrane proteins - PorA (*porA*-). Recombinant *Neisseria meningitidis* clones resulting from a double crossing over event (PCR screening using oligonucleotides **Cam-05** (5'-GTA CTG CGA TGA GTG GCA GG-3') & **proD15-52**) were selected on GC medium containing 5µg/ml chloramphenicol and analyzed for D15/Omp85 expression. As represented in Figure 10, the production of D15/Omp85 was significantly increased in the total protein extracts of *Nm* strains resulting from promoter replacement, when compared to parental strain (*cps*-). This result was also observed when analyzing outer-membrane blebs prepared from the same strains (see Figure 17). These results are attributable to the replacement of the endogenous *D15* promoter by the strong *porA* promoter. In addition, it was surprisingly found that expression, where the *porA* promoter was introduced approximately 400 bp upstream of the initiator codon, was approximately 50 times greater than when the promoter was placed approximately 100 bp upstream. Altogether, these experiments support that the promoter replacement strategy works and allows the up-regulation of the synthesis of integral outer-membrane proteins in outer-membrane blebs.

30

Certain geographically isolated human populations (such as Cuba) are infected by a limited number of *Neisseria meningitidis* isolates belonging largely to one or

few outer membrane protein serotypes. Since PorA is a major outer-membrane protein antigen which can induce protective and strain-specific bactericidal antibodies, it may be possible to confer vaccine protection in such a population using a limited number of porA serotypes. Moreover, PorA may interact with or stabilize some other outer  
5 membrane proteins. In this context, the presence of PorA in outer membrane vesicles may be advantageous, strengthening the vaccine efficacy of such recombinant improved blebs.

For such a reason, it may be desirable to up-regulate the expression of D15/Omp85 outer membrane protein in a *Neisseria meningitidis* serogroup B strain  
10 lacking functional *cps* genes but expressing PorA. Genomic DNA was extracted from the recombinant *Neisseria meningitidis* serogroup B *cps*-, *porA*-, D15/Omp85+ strain using the QIAGEN Genomic Tips 100-G kit. 10µgr of this material was linearized and used to transform *Neisseria meningitidis* serogroup B *cps*- following a classical transformation protocol. Recombinant *Neisseria* were obtained on GC agar plates  
15 containing 5µgr/ml chloramphenicol.

Integrations resulting from a double crossing-over upstream of the *D15* gene were screened by PCR as described previously. As homologous recombinations can occur everywhere in the chromosome, a second PCR screening was performed to control the integrity of the *porA* locus in the recombinant strain. For this purpose,  
20 internal *porA* primers PPA1 (5- GCG GCC GTT GCC GAT GTC AGC C -3') and PpA2 ( 5- GGC ATA GCT GAT GCG TGG AAC TGC -3' ) were used in a PCR screening experiment. The amplification of an 1170bp fragment confirms the presence of the *porA* gene in the recombinant bacteria.

Recombinant bacteria (corresponding to about  $5 \cdot 10^8$  bacteria) can be re-suspended in 50 µl of PAGE-SDS buffer, frozen(-20°C) / boiled (100°C) three times  
25 and then separated by PAGE-SDS electrophoresis on a 12.5 % gel. Gels can then be stained by Coomassie Brilliant blue R250 or transferred to a nitrocellulose membrane and probed either with an anti-porA monoclonal antibody or with an anti-D15/Omp85 rabbit polyclonal antibody. Analysis of outer-membrane blebs prepared from the same  
30 strains can also be performed.

**Example 11: Up-regulation of the Hsf protein antigen in a recombinant *Neisseria meningitidis* serogroup B strain lacking functional *cps* genes but expressing PorA.**

As described above, in certain countries, the presence of PorA in outer membrane vesicles may be advantageous, and can strengthen the vaccine efficacy of recombinant improved blebs. In the following example, we have used a modified pCMK(+) vector to up-regulate the expression of the Hsf protein antigen in a strain lacking functional *cps* genes but expressing PorA. The original pCMK(+) vector contains a chimeric *porA/lacO* promoter repressed in *E. coli* host expressing *lacIq* but transcriptionally active in *Neisseria meningitidis*. In the modified pCMK(+), the native *porA* promoter was used to drive the transcription of the *hsf* gene. The gene coding for Hsf was PCR amplified using the HSF 01-*NdeI* and HSF 02-*NheI* oligonucleotide primers, presented in the table below. Because of the sequence of the HSF 01-*NdeI* primer the Hsf protein expressed will contain two methionine residues at the 5' end. The conditions used for PCR amplification were those described by the supplier (HiFi DNA polymerase, Boehringer Mannheim, GmbH). Thermal cycling was the following: 25 times (94°C 1min., 48°C 1min., 72°C 3min.) and 1 time (72°C 10min., 4°C up to recovery). The corresponding amplicon was subsequently cloned in the corresponding restriction sites of pCMK(+) delivery vector. In this recombinant plasmid, designed pCMK(+)-Hsf, we deleted the *lacO* present in the chimeric *porA/lacO* promoter by a recombinant PCR strategy (See Figure 12). The pCMK(+)-Hsf plasmid was used as a template to PCR amplify 2 separate DNA fragments:

-fragment 1 contains the *porA* 5' recombinogenic region, the Kanamycin resistance gene and the *porA* promoter. Oligonucleotide primers used, RP1(*SacII*) and RP2, are presented in the table below. RP1 primer is homologous to the sequence just upstream of the *lac* operator.

-fragment 2 contains the Shine-Dalgarno sequence from the *porA* gene, the *hsf* gene and the *porA* 3' recombinogenic region. Oligonucleotide primers used, RP3 and RP4(*ApaI*), are presented in the table below. RP3 primer is homologous to the sequence just downstream of the *lac* operator. The 3' end of fragment 1 and the 5' end of fragment 2 have 48 bases overlapping. 500ng of each PCR (1 and 2) were used for a final PCR reaction using primers RP1 and RP4. The final amplicon obtained was subcloned in pSL1180 vector restricted with *SacII* and *ApaI*. The modified plasmid

pCMK(+)-Hsf was purified at a large scale using the QIAGEN maxiprep kit and 2 µg of this material was used to transform a *Neisseria meningitidis* serogroup B strain lacking functional *cps* genes (the strain described in example 1). In order to preserve the expression of *porA*, integration resulting from a single crossing-over was selected by a combination of PCR and Western blot screening procedures. Kanamycin resistant clones testing positive by *porA*-specific PCR and western blot were stored at -70°C as glycerol stocks and used for further studies. Bacteria (corresponding to about 5.10<sup>8</sup> bacteria) were re-suspended in 50 µl of PAGE-SDS buffer, frozen (-20°C) / boiled (100°C) three times and then were separated by PAGE-SDS electrophoresis on a 12.5 % gel. The expression of Hsf was examined in Whole-cell bacterial lysates (WCBL) derived from *NmB* [Cps-, PorA+] or *NmB* [Cps-, PorA+, Hsf+]. Coomassie staining detected a significant increase in the expression of Hsf (with respect to the endogenous Hsf level) (See in Figure 13). This result confirms that the modified pCMK(+)-Hsf vector is functional and can be used successfully to up-regulate the expression of outer membrane proteins, without abolishing the production of the major PorA outer membrane protein antigen.

#### 20 Oligonucleotides used in this work

Oligonucleotides	Sequence	Remark(s)
Hsf 01-Nde	5'- GGA ATT CCA TAT GAT GAA CAA AAT ATA CCG C-3'	<i>Nde</i> I cloning site
Hsf 02-Nhe	5'-GTA GCT AGC TAG CTT ACC ACT GAT AAC CGA C-3'	<i>Nhe</i> I cloning site
GFP-mut-Asn	5'-AAC TGC AGA ATT AAT ATG AAA GGA GAA GAA CTT TTC-3'	<i>Asn</i> I cloning site Compatible with <i>Nde</i> I
GFP-Spe	5'-GAC ATA CTA GTT TAT TTG TAG AGC TCA TCC ATG -3'	<i>Spe</i> I cloning site Compatible with <i>Nhe</i> I
RP1 (SacII)	5'- TCC CCG CGG GCC GTC TGA ATA CAT CCC GTC-3'	<i>Sac</i> II cloning site
RP2	5'-CAT ATG GGC TTC CTT TTG TAA ATT TGA GGG CAA ACA CCC GAT ACG TCT TCA-3'	

RP3	5'-AGA CGT ATC GGG TGT TTG CCC TCA AAT TTA CAA AAG GAA GCC CAT ATG -3'	
RP4(ApaI)	5'-GGG TAT TCC GGG CCC TTC AGA CGG CGC AGC AGG -3'	<i>ApaI</i> cloning site

**Example 12:** Expression of the Green Fluorescent Protein in a recombinant *Neisseria meningitidis* serogroup B strain lacking functional *cps* genes but expressing *PorA*.

5 In the following example, the pCMK vector was used to test the expression of a cytoplasmic heterologous protein in *Neisseria meningitidis*. The Green Fluorescent Protein was amplified from the pKen-Gfpmut2 plasmid with the primers GFP-Asn-mut2 and GFP-Spe (see table in Example 11). *AsnI* gives cohesive ends compatible with *NdeI*, *SpeI* gives cohesive ends compatible with *NheI*. The conditions used for  
10 PCR amplification were those described by the supplier (HiFi DNA polymerase, Boehringer Mannheim, GmbH). Thermal cycling was the following: 25 times (94°C 1min., 48°C 1min., 72°C 3min.) and 1 time (72°C 10min., 4°C up to recovery). The corresponding amplicon was subsequently cloned in the pCMK(+) delivery vector digested with *NdeI* and *NheI* restriction enzymes. In this recombinant plasmid,  
15 designed pCMK(+)-GFP, we deleted the *lacO* present in the chimeric *porA/lacO* promoter by a recombinant PCR strategy. The pCMK(+)-GFP plasmid was used as template to PCR amplify 2 separate DNA fragments:

-fragment 1 contained the *porA* 5' recombinogenic region, the Kanamycin resistance gene and the *porA* promoter. Oligonucleotide primers used, RP1(*SacII*) and  
20 RP2 (see table in example 11). RP1 primer is homologous to the sequence just upstream of the *lac* operator.

-fragment 2 contains the *PorA* Shine-Dalgarno sequence, the *gfp* gene and the *porA* 3' recombinogenic region. Oligonucleotide primers used, RP3 and RP4(*ApaI*), are presented in the table in example 11. RP3 primer is homologous to the sequence  
25 just downstream of the *lac* operator.

The 3'end of fragment 1 and the 5'end of fragment 2 have 48 bases overlapping. 500ng of each PCR (1 and 2) were used for a final PCR reaction using

primers RP1 and RP4. Twenty  $\mu$ g of this PCR fragment were used to transform a *Neisseria meningitidis* serogroup B strain lacking functional *cps* genes.

Transformation with linear DNA is less efficient than with circular plasmid DNA but all the recombinants obtained performed a double crossing-over (confirmed by a combination of PCR and Western blot screening procedures). Kanamycin resistant clones were stored at  $-70^{\circ}\text{C}$  as glycerol stocks and used for further studies. Bacteria (corresponding to about  $5.10^8$  bacteria) were re-suspended in 50  $\mu$ l of PAGE-SDS buffer, frozen ( $-20^{\circ}\text{C}$ ) / boiled ( $100^{\circ}\text{C}$ ) three times and then were separated by PAGE-SDS electrophoresis on a 12.5 % gel.

The expression of GFP was examined in Whole-cell bacterial lysates (WCBL) derived from *NmB* [Cps-, PorA+] or *NmB* [Cps-, PorA-, GFP+]. Coomassie staining detected an expression of GFP absent in the recipient *Neisseria meningitidis* strain (see figure 14).

**Example 13: Up-regulation of the *N. meningitidis* serogroup B *NspA* gene by promoter replacement**

The aim of the experiment was to replace the endogenous promoter region of the *NspA* gene by the strong *porA* promoter, in order to up-regulate the production of the NspA antigen. For that purpose, a promoter replacement plasmid was constructed using *E. coli* cloning methodologies. A DNA region (924bp) located upstream from the *NspA* coding gene was discovered (SEQ ID NO: 7) in the private Incyte PathoSeq data base containing unfinished genomic DNA sequences of the *Neisseria meningitidis* strain ATCC 13090. A DNA fragment (675bp) covering nucleotides -115 to -790 with respect to the *NspA* gene start codon (ATG) was PCR amplified using oligonucleotides PNS1' (5'-CCG CGA ATT CGA CGA AGC CGC CCT CGA C-3') and PNS2 (5'-CGT CTA GAC GTA GCG GTA TCC GGC TGC -3') containing *EcoRI* and *XbaI* restriction sites (underlined) respectively. The PCR fragment was submitted to restriction with *EcoRI* and *XbaI* and inserted in pUC18. This plasmid was submitted to circle PCR mutagenesis (Jones & Winistofer (1992), Biotechniques12: 528-534) in order to insert meningococcal uptake sequences required for transformation, and suitable restriction sites allowing cloning of a *CmR*/*PorA* promoter cassette. The circle PCR was performed using the

**BAD01-2** (5'- GGC GCC CGG GCT CGA GCT TAT CGA TGG AAA ACG CAG C-3') & **BAD02-2** (5'-GGC GCC CGG GCT CGA GTT CAG ACG GCG CGC TTA TAT AGT GGA TTA AC -3') oligonucleotides containing uptake sequences and suitable restriction sites (*Xma*I and *Xho*I) underlined. The resulting PCR fragment was gel-purified and digested with *Xho*I. The *CmR*/PorA promoter cassette was amplified from the pUC D15/Omp85 plasmid previously described, using primers

**BAD 15-2** (5'-GGC GCC CGG GCT CGA GTC TAG ACA TCG GGC AAA CAC CCG-3') & **BAD 03-2** (5'- GGC GCC CGG GCT CGA GCA CTA GTA TTA CCC TGT TAT CCC-3') oligonucleotides containing suitable restriction sites (*Xma*I, *Xba*I, *Spe*I and *Xho*I) underlined. The PCR fragment obtained was submitted to digestion and inserted in the circle PCR plasmid restricted with the corresponding enzymes. 10 µg of the recombinant plasmid were linearized and used to transform a strain of *Neisseria meningitidis* serogroup B lacking capsular polysaccharide (*cps*-) and one of the major outer membrane proteins - PorA (*porA*-). Recombinant *Neisseria meningitidis* clones resulting from a double crossing over event (PCR screening using oligonucleotides **BAD 25** (5'-GAG CGA AGC CGT CGA ACG C -3') & **BAD08** (5'-CTT AAG CGT CGG ACA TTT CC-3')) were selected on GC agar plates containing 5µg/ml chloramphenicol and analyzed for NspA expression. Recombinant bacteria (corresponding to about  $5 \cdot 10^8$  bacteria) were re-suspended in 50 µl of PAGE-SDS buffer, frozen (-20°C) / boiled (100°C) three times and then were separated by PAGE-SDS electrophoresis on a 12.5 % gel. Gels were then stained by Coomassie Brilliant blue R250 or transferred to a nitrocellulose membrane and probed either with an anti-PorA monoclonal antibody or with anti-NspA polyclonal antibody (figure 17). As for Omp85, there is a surprising indication that insertion of the promoter approximately 400 bp upstream of the NspA initiation codon expresses more protein than if placed approximately 100 bp upstream.

The same recombinant pUC plasmid can be used to up-regulate the expression of NspA in a *Neisseria meningitidis* serogroup B strain lacking functional *cps* gene but still expressing PorA.



**Example 14: Up-regulation of the *N. meningitidis* serogroup B *pldA* (*omplA*) gene by promoter replacement.**

The aim of the experiment was to replace the endogenous promoter region of the *pldA* (*omplA*) gene by the strong *porA* promoter in order to up-regulate the production of the PldA (OmplA1) antigen. For that purpose, a promoter replacement plasmid was constructed using *E. coli* cloning methodologies. A DNA region (373bp) located upstream from the *pldA* coding sequence was discovered (SEQ ID NO: 18) in the private Incyte PathoSeq data base of the *Neisseria meningitidis* strain ATCC 13090. This DNA contains the sequence coding for a putative *rpsT* gene. The stop codon of *rpsT* is located 169bp upstream the *pldA* ATG. To avoid the disruption of this potentially important gene, we decided to insert the *CmR/PorA* promoter cassette just upstream of the ATG of *pldA*. For that purpose, a DNA fragment of 992 bp corresponding to the the *rpsT* gene, the 169 bp intergenic sequence and the 499 first nucleotides of *pldA* gene was PCR amplified from *Neisseria meningitidis* serogroup B genomic DNA using oligonucleotides **PLA1 Amo5** (5'-GCC GTC TGA ATT TAA AAT TGC GCG TTT ACA G-3') and **PLA1 Amo3** (5'-GTA GTC TAG ATT CAG ACG GCG CAA TTT GGT TTC CGC AC -3') containing uptake sequences (underlined). PLA1 Amo3 contains also a *XbaI* restriction site. This PCR fragment was cleaned with a High Pure Kit (Roche, Mannheim, Germany) and directly cloned in a pGemT vector (Promega, USA). This plasmid was submitted to circle PCR mutagenesis (Jones & Winistofer (1992)) in order to insert suitable restriction sites allowing cloning of a *CmR/PorA* promoter cassette. The circle PCR was performed using the **CIRC1-Bgl** (5'CCT AGA TCT CTC CGC CCC CCA TTG TCG -3') & either **CIRC1-XH-RBS/2** (5'-CCG CTC GAG TAC AAA AGG AAG CCG ATA TGA ATA TAC GGA ATA TGC G-3') or **CIRC2-XHO/2** (5'-CCG CTC GAG ATG AAT ATA CGG AAT -3') oligonucleotides containing suitable restriction sites (*Bgl*II and *Xho*I) underlined. The *CmR/PorA* promoter cassette was amplified from the pUC D15/Omp85 plasmid previously described, using primers **BAD20** (5'- TCC CCC GGG AGA TCT CAC TAG TAT TAC CCT GTT ATC CC-3') and **CM-PORA-3** (5'- CCG CTC GAG ATA AAA ACC TAA AAA CAT CGG GC-3') containing suitable restriction sites (*Bgl*II and *Xho*I) underlined. This PCR fragment was cloned

in the circle PCR plasmid obtained with primers CIRC1-Bgl and CIRC1-XH-RBS/2. This plasmid can be used to transform *Neisseria meningitidis* serogroup B (*cps*-) and (*cps*- *porA*-) strains. Integration by double crossing-over in the upstream region of *pldA* will direct the insertion of the *porA* promoter directly upstream of the *pldA* ATG.

5 Another cassette was amplified from the genomic DNA of the recombinant *Neisseria meningitidis* serogroup B (*cps*-, *porA*-, D15/Omp85+) over-expressing D15/Omp85 by promoter replacement. This cassette contains the *cmR* gene, the *porA* promoter and 400bp corresponding to the 5' flanking sequence of the *D15/Omp85* gene. This sequence has been proven to be efficacious for up-regulation of the expression of

10 D15/Omp85 in *Neisseria* and will be tested for the up-regulation of the expression of other *Neisseria* antigens. Primers used for the amplification were **BAD 20** and **CM-PORA-D15/3** (5'- CGG CTC GAG TGT CAG TTC CTT GTG GTG C-3') containing *XhoI* restriction sites (underlined). This PCR fragment was cloned in the circle PCR plasmid obtained with primers CIRC1-Bgl and CIRC2-XHO/2. This

15 plasmid will be used to transform *Neisseria meningitidis* serogroup B (*cps*-) and (*cps*-, *porA*-) strains. Integration by double crossing-over in the upstream region of *pldA* will direct the insertion of the *porA* promoter 400bp upstream the *pldA* ATG.

**Example 15: Up-regulation of the *N. meningitidis* serogroup B *tbpA* gene by promoter replacement.**

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The aim of the experiment was to replace the endogenous promoter region of the *tbpA* gene by the strong *porA* promoter, in order to up-regulate the production of the TbpA antigen. For that purpose, a promoter replacement plasmid was constructed using *E. coli* cloning methodologies. A DNA region (731bp) located upstream from

25 the *tbpA* coding sequence was discovered (SEQ ID NO: 17) in the private Incyte PathoSeq data base of the *Neisseria meningitidis* strain ATCC 13090. This DNA contains the sequence coding for TbpB antigen. The genes are organized in an operon. The *tbpB* gene will be deleted and replaced by the *CmR/porA* promoter cassette. For that purpose, a DNA fragment of 3218bp corresponding to the 509bp 5' flanking

30 region of *tbpB* gene, the 2139bp *tbpB* coding sequence, the 87bp intergenic sequence and the 483 first nucleotides of *tbpA* coding sequence was PCR amplified from *Neisseria meningitidis* serogroup B genomic DNA using oligonucleotides **BAD16** (5'-

GGC CTA GCT AGC CGT CTG AAG CGA TTA GAG TTT CAA AAT TTA TTC-3') and **BAD17** (5'-GGC CAA GCT TCA GAC GGC GTT CGA CCG AGT TTG AGC CTT TGC-3') containing uptake sequences and *NheI* and *HindIII* restriction sites (underlined). This PCR fragment was cleaned with a High Pure Kit (Boehringer Mannheim, Germany) and directly cloned in a pGemT vector (Promega, USA). This plasmid was submitted to circle PCR mutagenesis (Jones & Winistofer (1992)) in order to (i) insert suitable restriction sites allowing cloning of a *CmR/PorA* promoter cassette and (ii) to delete 209bp of the 5' flanking sequence of *tbpB* and the *tbpB* coding sequence. The circle PCR was performed using the **BAD 18** (5'-TCC CCC GGG AAG ATC TGG ACG AAA AAT CTC AAG AAA CCG-3') & the **BAD 19** (5'-GGA AGA TCT CCG CTC GAG CAA ATT TAC AAA AGG AAG CCG ATA TGC AAC AGC AAC ATT TGT TCC G -3') oligonucleotides containing suitable restriction sites *XmaI*, *BglII* and *XhoI* (underlined). The *CmR/PorA* promoter cassette was amplified from the pUC D15/Omp85 plasmid previously described, using primers **BAD21** (5'- GGA AGA TCT CCG CTC GAG ACA TCG GGC AAA CAC CCG-3') & **BAD20** (5'- TCC CCC GGG AGA TCT CAC TAG TAT TAC CCT GTT ATC CC-3') containing suitable restriction sites *XmaI*, *SpeI*, *BglII* and *XhoI* (underlined). This PCR fragment was cloned in the circle PCR plasmid. This plasmid will be used to transform *Neisseria meningitidis* serogroup B (*cps-*) and (*cps- porA-*) strains. Integration by double crossing-over in the upstream region of *tbpA* will direct the insertion of the *porA* promoter directly upstream of the *tbpA* ATG.

**Example 16: Up-regulation of the *N. meningitidis* serogroup B *pilQ* gene by promoter replacement.**

The aim of the experiment was to replace the endogenous promoter region of the *pilQ* gene by the strong *porA* promoter, in order to up-regulate the production of the PilQ antigen. For that purpose, a promoter replacement plasmid was constructed using *E. coli* cloning methodologies. A DNA region (772bp) located upstream from the *pilQ* coding gene was discovered (SEQ ID NO: 12) in the private Incyte PathoSeq data base of the *Neisseria meningitidis* strain ATCC 13090. This DNA contains the sequence coding for PilP antigen. The *pilQ* gene is part of an operon we do not want to disturb, pilins being essential elements of the bacteria. The *CmR/porA* promoter

cassette was introduced upstream the *pilQ* gene following the same strategy described for the up-regulation of the expression of the *pldA* gene. For that purpose, a DNA fragment of 866 bp corresponding to the 3' part of the *pilP* coding sequence, the 18bp intergenic sequence and the 392 first nucleotides of *pilQ* gene was PCR amplified from *Neisseria* serogroup B genomic DNA using **PQ-rec5-Nhe** (5'-CTA GCT AGC GCC GTC TGA ACG ACG CGA AGC CAA AGC-3') and **PQ-rec3-Hin** (GCC AAG CTT TTC AGA CGG CAC GGT ATC GTC CGA TTC G-3') oligonucleotides containing uptake sequences and *NheI* and *HindIII* restriction sites (underlined). This PCR fragment was directly cloned in a pGemT vector (Promega, USA). This plasmid was submitted to circle PCR mutagenesis (Jones & Winistofer (1992)) in order to insert suitable restriction sites allowing cloning of a *CmR*/*PorA* promoter cassette. The circle PCR was performed using the **CIRC1-PQ-Bgl** (5'-GGA AGA TCT AAT GGA GTA ATC CTC TTC TTA-3') & either **CIRC1-PQ-XHO** (5'-CCG CTC GAG TAC AAA AGG AAG CCG ATA TGA TTA CCA AAC TGA CAA AAA TC-3') or **CIRC2-PQ-X** (5'-CCG CTC GAG ATG AAT ACC AAA CTG ACA AAA ATC -3') oligonucleotides containing suitable restriction sites *Bgl*II and *Xho*I (underlined). The *CmR*/*PorA* promoter cassette was amplified from the pUC D15/*Omp85* plasmid previously described, using primers **BAD20** (5'- TCC CCC GGG AGA TCT CAC TAG TAT TAC CCT GTT ATC CC-3') and **CM-PORA-3** (5'- CCG CTC GAG ATA AAA ACC TAA AAA CAT CGG GCA AAC ACC C-3') containing suitable restriction sites *Bgl*II and *Xho*I (underlined). This PCR fragment was cloned in the circle PCR plasmid obtained with primers CIRC1-PQ-Bgl and CIRC1-PQ-XHO. This plasmid can be used to transform *Neisseria meningitidis* serogroup B (*cps*-) and (*cps*-, *porA*-) strains. Integration by double crossing-over in the upstream region of *pilQ* will direct the insertion of the *porA* promoter directly upstream of the *pilQ* ATG.

Another cassette was amplified from the genomic DNA of the recombinant *Neisseria meningitidis* serogroup B (*cps*-, *porA*-, *D15/Omp85*+) over-expressing *D15/Omp85* by promoter replacement. This cassette contains the *cmR* gene, the *porA* promoter and 400bp corresponding to the 5' flanking sequence of the *D15/Omp85* gene. This sequence has been proven to be efficacious for up-regulation of the expression of *D15/Omp85* in *Neisseria meningitidis* and will be tested for the up-regulation of the expression of other *Neisseria* antigens. Primers used for the

amplification were **BAD 20** and **CM-PORA-D153** (5'- GGG CTC GAG TGT CAG TTC CTT GTG GTG C-3') containing *XhoI* restriction sites (underlined). This PCR fragment was cloned in the circle PCR plasmid obtained with primers CIRC1-PQ-Bgl and CIRC2-PQ-X. This plasmid can be used to transform *Neisseria meningitidis* serogroup B [*cps*-] and [*cps*-, *porA*-] strains. Integration by double crossing-over in the upstream region of *pilQ* will direct the insertion of the *porA* promoter 400bp upstream the *pilQ* ATG.

**Example 17: Construction of a *kanR/sacB* cassette for introducing "clean", unmarked mutations in the *N. meningitidis* chromosome.**

The aim of the experiment is to construct a versatile DNA cassette containing a selectable marker for the positive screening of recombination in the chromosome of *Neisseria meningitidis* (ie: *kanR* gene), and a counter selectable marker to delete the cassette from the chromosome after recombination (ie: *sacB* gene). By this method, any heterologous DNA introduced during homologous recombination will be removed from the *Neisseria* chromosome.

A DNA fragment containing the *neoR* gene and the *sacB* gene expressed under the control of its own promoter was obtained by restriction of the pIB 279 plasmid (Blomfield IC, Vaughn V, Rest RF, Eisenstein BI (1991), Mol Microbiol 5:1447-57) with *BamHI* restriction enzyme. The recipient vector was derived from plasmid pCMK, previously described. The *kanR* gene of the pCMK was deleted by restriction with enzymes *NruI* and *EcoRV*. This plasmid was named pCMKs. The *neoR/sacB* cassette was inserted in the pCMKs at a *BglIII* restriction site compatible with *BamHI* ends.

*E. coli* harboring the plasmid is unable to grow in the presence of 2% sucrose in the culture medium, confirming the functionality of the *sacB* promoter.

This plasmid contains recombinogenic sequences allowing the insertion of the cassette at the *porA* locus in the chromosome of *Neisseria meningitidis* serogroup B. Recombinant *Neisseria* were obtained on GC agar plates containing 200µg/ml of kanamycin. Unfortunately, the *sacB* promoter was not functional in *Neisseria meningitidis*: no growth difference was observed on GC agar plates containing 2% sucrose.

A new cassette was constructed containing the *sacB* gene under the control of the *kanR* promoter. A circle PCR was performed using the plasmid pUC4K ((Amersham Pharmacia Biotech, USA)) as a template with **CIRC-Kan-Nco** (5'-CAT GCC ATG GTT AGA AAA ACT CAT CGA GCA TC-3') & **CIRC-Kan-Xba** (5'-CTA GTC TAG ATC AGA ATT GGT TAA TTG GTT G-3') oligonucleotides containing *NcoI* and *XbaI* restriction sites (underlined). The resulting PCR fragment was gel-purified, digested with *NcoI* and ligated to the *sacB* gene generated by PCR from the pIB279 plasmid with **SAC/NCO/NEW5** (5'-CAT GCC ATG GGA GGA TGA ACG ATG AAC ATC AAA AAG TTT GCA A-3') oligonucleotide containing a *NcoI* restriction site (underlined) and a RBS (bold) & **SAC/NCO/NEW3** (5'-GAT CCC ATG GTT ATT TGT TAA CTG TTA ATT GTC-3') oligonucleotide containing a *NcoI* restriction site (underlined). The recombinant *E. coli* clones can be tested for their sensitivity on agar plates containing 2% sucrose. The new *kanR/sacB* cassette can be subcloned in the pCMKs and used to transform a *Neisseria meningitidis* serogroup B *cps*- strain. The acquired sucrose sensitivity will be confirmed in *Neisseria*. The pCMKs plasmid will be used to transform the recombinant *kanR/SacB Neisseria* to delete the entire cassette inserted in the chromosome at the *porA* locus. Clean recombinant *Neisseria* will be obtained on GC agar plates containing 2% sucrose.

**Example 18: Use of small recombinogenic sequences (43bp) to allow homologous recombination in the chromosome of *Neisseria meningitidis*.**

The aim of the experiment is to use small recombinogenic sequences (43bp) to drive insertions, modifications or deletions in the chromosome of *Neisseria*. The achievement of this experiment will greatly facilitate future work, in terms of avoiding subcloning steps of homologous sequences in *E. coli* (recombinogenic sequences of 43bp can easily be added in the PCR amplification primer). The *kanR* gene was PCR amplified from plasmid pUC4K with oligonucleotides **Kan-PorA-5** (5'-GCC GTC TGA ACC CGT CAT TCC CGC GCA GGC GGG AAT CCA GTC CGT TCA GTT TCG GGA AAG CCA CGT TGT GTC-3') containing 43bp homologous to the 5' flanking sequence of *NmB porA* gene (bold) and an uptake sequence (underlined) & **Kan-PorA-3** (5'-TTC AGA CGG CGC AGC AGG AAT

TTA TCG GAA ATA ACT GAA ACC GAA CAG ACT AGG CTG AGG TCT  
GCC TCG-3') containing 43bp homologous to the 3' flanking sequence of *NmB porA*  
gene (bold) and an uptake sequence (underlined). The 1300bp DNA fragment  
obtained was cloned in pGemT vector (Promega, USA). This plasmid can be used to  
transform a *Neisseria meningitidis* serogroupB *cps*- strain. Recombinant *Neisseria*  
will be obtained on GC plates containing 200µg/ml kanamycin. Integrations resulting  
from a double crossing-over at the *porA* locus will be screened by PCR with primers  
PPA1 & PPA2 as described previously.

**Example 19: Active protection of mice immunized with WT and recombinant *Neisseria meningitidis* blebs**

Animals were immunised three times (IP route) with 5 µg of the different  
OMVs adsorbed on Al(OH)<sub>3</sub> on days 0, 14 and 28. Bleedings were done on days 28  
(day 14 Post II) and 35 (day 7 post III), and they were challenged on day 35 (IP  
route). The challenge dose was 20 x LD<sub>50</sub> (~10<sup>7</sup> CFU/mouse). Mortality rate was  
monitored for 7 days after challenge.

OMVs injected were:

Group1: Cps-, PorA+ blebs

Group2: Cps-, PorA- blebs

Group3: Cps-, PorA-, NspA+ blebs

Group4: Cps-, PorA-, Omp85+ blebs

Group5: Cps-, PorA-, Hsf+ blebs

Figure 15 illustrates the pattern of these OMVs by analyzed SDS Page  
(Coomassie staining).

24 hours after the challenge, there was 100% mortality (8/8) in the negative  
control group (immunised with Al(OH)<sub>3</sub> alone) while mice immunised with the 5  
different OMVs preparations were still alive (7 to 8/8 mice survived). Sickness was  
also monitored during the 7 days and the mice immunised with the NSPA over-  
expressed blebs appeared to be less sick than the other groups. PorA present in PorA+  
blebs is likely to confer extensive protection against infection by the homologous  
strain. However, protection induced by PorA- up-regulated blebs is likely to be due at  
least to some extent, to the presence of increased amount of NspA, Omp85 or Hsf.

**Example 20: Immunogenicity of recombinant blebs measured by whole cell & specific ELISA methods**

To measure the ability of the antibodies to recognize the antigens present on the MenB cell surface, the pooled mice sera (from Example 19) were tested by whole cell ELISA (using tetracyclin inactivated cells), and titers were expressed as mid-point titers. All types of bleb antibodies induce a high whole cell Ab titer while the negative control group was clearly negative.

Blebs	WCE(H44/76) mid-point titer	
	14P2	14P3
CPS(-) PorA(+)	23849	65539
CPS(-) PorA(-)	20130	40150
CPS(-) PorA(-) NSPA(+)	8435	23846
CPS(-) PorA(-) OMP85(+)	4747	16116
CPS(-) PorA(-) HSF(+)	6964	22504
(-)	51	82

10

The specific Ab response to available recombinant HSF protein was carried out. Microplates were coated with 1 µg/ml full length HSF molecule.

The results illustrated in Figure 16 show that there was a good specific HSF response when HSF over-expressed OMVs were used to immunize mice (using purified recombinant HSF on the plates). The HSF over-expressed blebs induce a good level of specific antibodies.

15



## SEQ. ID NO:1

## Nucleotide sequence of the pCMK(+) vector

TCTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGT  
AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA  
5 AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG  
TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCCT  
GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCA  
GTTCCGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGT  
AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC  
10 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCT  
GCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGT  
GGTTTTTTTGGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC  
TGACGCTCAGTGAACGAAACTCAGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACTAGATCCTTT  
TAAATTAAGAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGT  
15 GAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCTGACTCCCCGTCGTGTAGATAACTACGATACG  
GGAGGGCTTACCATCTGGCCCCAGTCTGCAATGATACCGCGAGACCCACGCTCACCAGCTCCAGATTTATCAGCAATAA  
ACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTTGTGCGCG  
GAAGCTAGAGTAAGTAGTTTCGCGAGTTAATAGTTTGCACGACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTC  
GTGTTTTGGTATGGCTTCATTGAGCTCCGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAG  
20 CGGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAAGTTGGCGCAGTGTATCACTCATGTTATGGCAGCACTG  
CATAATTCTCTTACTGTGATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATA  
GTGTATGCGCGACCGAGTTGCTCTTGCCTCGCGCTCAATACGGGATAATACCGCGCCATAGCAGAACTTTAAAGTGC  
TCATCATTTGGAAGACGTTCTTCGGGCGCAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACT  
CGTGACCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAACAGGAAGGCAAAATGCCGC  
25 AAAAAAGGGAATAAGGGCGACACGGAATGTTGAATACTCATACTCTTCTCTTTTCAATATTATTGAAGCATTATCAGG  
GTTATTGTCTCATGAGCGGATACATATTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCGCA  
AAAGTGCCACCTGACGCTCTAAGAAACCATTAATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTCG  
TCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGG  
ATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGCGGGGTGTCGGGGCTGGCTTAACTATGCGGCATCA  
30 GAGCAGATTGTACTGAGAGTGACCATATAAATTTGAACGTTAATATTTTGTAAAAATTCGCGTTAAATTTTGTAAAT  
CAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGCCCGAGATAGGGTTGAGTG  
TTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAAGCTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGC  
GATGGCCCACTACGTGAACCATCACCAATCAAGTTTTTGGGGTTCGAGGTGCGGTAAAGCACTAAATCGGAACCTTAA  
AGGGAGCCCCGATTTAGAGCTTGACGGGAAAGCCGCGCAACGTTGCGAGAAAGGAAGGAAGAAAGCGAAAGGAGCGG  
35 GCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCGCGCTTAATGCGCCGCTACAGGGC  
GCGTACTATGGTTGCTTTGACGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGCGCCAT  
TCGCCATTACAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG  
ATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCAGTCACGACGTTGTAACGACGCGCCAGTGCCAAGC  
TTGCCGTCTGAATACATCCCGTCATTCCTCAAAAAACAGAAAAACCAAAATCAGAAACCTAAATCCCGTCATTCCCGCGCA  
40 GCGGGAATCCAGTCCGTTTCAGTTTCGGTCATTTCGATAAATTCCTGCTGCTTTTCATTCTAGATTCCCACTTTTCGTG  
GGAATGACGGCGGAAGGGTTTTGGTTTTTCCGATAAATCTTGAGGCATTGAAATTTAGATTCCCGCTGCGCGGGAA  
TGACGGCTGTAGATGCCGATGGTCTTTATAGCGGATTACAAAAATCAGGACAAGGCGACGAAGCCGACAGTACAG  
ATAGTACGGAACCGATTCACTTGGTGTTCAGCACCTTAGAGAATCGTTCTCTTTGAGCTAAGGCGAGGCAACGCCGTAC  
TTGTTTTTGTAAATCCACTATAAAGTGCGCGTGTGTTTTTTATGGCGTTTTAAAAAGCCGAGACTGCATCCGGGCGAGC  
45 AGCGCATCGGCCCGACGAGGTCTCTGGAGTCGCGAGCATCAAGGGCGAATTCGTCAGGGGGGGGGGAAAGCCAGTT  
GTGTCTCAAAATCTCTGATGTACATTGCACAAGATAAAAAATATATCATCATGAACAATAAACTGTCTGCTTACATAAA  
CAGTAATACAAGGGGTGTTATGAGCCATATTCAACGGGAAACGTCCTTGCTCGAGGCCGCGATTAAATTCACATCGGATG

CTGATTATATGGGTATAAATGGGCTCGCGATAATGTCTGGGCAATCAGGTGCGACAATCTATCGATTGTATGGGAAGCCC  
GATGCGCCAGAGTTGTTTCTGAAACATGGCAAAGGTAGCGTTGCCAATGATGTTACAGATGAGATGGTCAGACTAAACTG  
GCTGACGGAATTTATGCTCTTCCGACCATCAAGCATTTTATCCGTACTCTCTGATGATGCGTGGTTACTCACCCTGCGA  
TCCCCGGGAAAAACAGCATTCCAGGTATTAGAAGAATATCCTGATTACAGGTGAAAATATTGTTGATGCGCTGGCAGTGTTT  
5 CTGCGCCGGTTGCATTTCGATTCTGTTTGTAAATGTCTTTTAAACAGCGATCGCGTATTTCTGCTCGCTCAGGCGCAATC  
ACGAATGAATAACGGTTTGGTTGATGCGAGTGATTTTGTATGACGAGCGTAATGGCTGGCCTGTTGAACAAGTCTGGAAG  
AAATGCATAAGCTTTTGCCATTCTCACCAGATTCACTCGTCACTCATGGTGATTTCTCACTTGATAACCTTATTTTGTAC  
GAGGGGAAATTAATAGGTTGTATTGATGTTGGACGAGTCGGAATCGCAGACCGATACCAGGATCTTGCCATCTTATGGAA  
CTGCTCGGTGAGTTTCTCTTCACTACAGAAACGGCTTTTCAAAAAATATGGTATTGATAATCCTGATATGAATAAAT  
10 TGCAGTTTCATTTGATGCTCGATGAGTTTCTAATCAGAATTGGTTAATTGGTTGTAACACTGGCAGAGCATTACGCTG  
ACTTGACGGGACGGCGGCTTTGTGAATAAATCGAATTTTGTCTGAGTTGAAGGATCAGATCACGCATCTTCCCGACAAC  
GCAGACCGTTCCGTGGCAAAGCAAAGTTCAAAATCACCACTGGTCCACCTACAACAAAGCTCTCATCAACCGTGCGTC  
CCTCACTTTCTGCTGGATGATGGGGCGATTAGGCTGTTGATGAGTCAGCAACACCTTCTTACGAGGCGAGCCTCAGC  
GCCCCCCCCCTGCGAGGCTGCGCTTGAAATGTGTTGTAGAAACACAACGTTTGTGAAAAATAAGCTATTGTTT  
15 TATATCAAAATATAATCATTTTAAAAATAAGGTTGCGGCATTTATCAGATATTGTTCTGAAAAATGGTTTTTTCGGG  
GGGGGGGTATAATTGAAGACGTATCGGGTGTGTCGGGAATTGTGAGCGGATAACAATTCGATGTTTTTAGGTTTTTA  
TCAATTTTACAAAAGGAAGCCCATATGCATCCTAGGCCTATTAATATTCGGAGTATACGTAGCCGGCTAACGTTAACAA  
CCGTACTCTAGAACTATAGCTAGCATGCGCAAATTTAAAGCGCTGATATCGATCGCGCGCAGATCTGATTAAATAGGC  
GAAATACAGCTACGATCAAATCATCGCGCGGTTGATTATGATTTTCCAAACGCCTTCCGCCATCGTGTCTGGCGC  
20 TTGGCTGAAACGCAATACCGGCATCGGCACTACACTCAAATTAATGCCGCTCCGTGCGTTTGGCCACAAATCTAAA  
TATCGGGCGGTGAAGCGGATAGCTTTGTTTTGACGGCTTCGCCTTCATTCTTTGATTGCAATCTGACTGCCAATCTGC  
TTCAGCCCCAAACAAAAACCGGATACGGAAGAAAAACGCAATAAAGACAGCAAATACCGTCTGAAAGATTTTCAGACG  
GTATTTTCGATTTTGGCTTGGTTTGACATATAGTGAGACCTTGGCAAAAATAGTCTGTTAACGAAAATTTGACGCATAA  
AAATGCGCAAAAAATTTCAATTGCCTAAAACTTCTTAATATTGAGCAAAAAGTAGGAAAAATCAGAAAAGTTTGGCA  
25 TTTTGAAAAATGAGATTGAGCATAAAATTTTAGTAACCTATGTTATTGCAAAGGTCTCGAATTGTCATTCCCACGAGGCG  
GGAATCTAGTCTGTTTCGGTTTCAGTTATTTCCGATAAATCCTGCTGCGCCGTCTGAAGAATTCTGAATCATGTCATAG  
CTGTTTCTGTGTGAAATTGTTATCCGCTCACAATTCACACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGG  
TGCTTAATGAGTGAGCTAACTCACATTAATGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGC  
TGCATTAATGAATCGGCCAACGCGCGGGAGAGCGGTTTGCGTATTGGGCGC  
30

SEQ. ID NO:2

**Nucleotide sequence of DNA region (997 bp) up-stream from the NspA gene in the *Neisseria meningitidis* serogroup A strain Z2491.**

GGAACCGAACACGCGTTTCGGTCATACGCCGCCGAAAGGTTTGGCCGAAGACGAAGCCGCCCTCGACATCGAAGACGCGG  
35 TACACGGCGCGCTGGAAGCGCGGTTTGTCCACTACGAAACATCGGCTTTTGGCAAACAGCCATGCAGTGCCGCCAC  
AATTTGAACTACTGGCAGTTTCGGCGATTATTTAGGCATAGGCGCGGCGCGCACGGCAAAATTTCTATCCCGACCGCAT  
CGAGCGCACCGTCCGCCGCCGCCACCCCAACGACTACCTCGCCTTAATGCAAAACCGACCGAGCGAAGCCGTGCAACGCA  
AAACCGTCGCGCGCGAAGATTGCGGTTTGAATTCATGATGAACGCCCTGCGCCTGACCGACGGCGTACCCACCGCGATG  
TTGCAGGAGCGCACGGGCGTACCGAGTGCCAAAATCATGGCGCAAATCGAAACGGCAAGGCAAAAAGGCTGCTGGAAC  
40 CGACCCCGCGTATTCGCCCGACCGAAAAAGACGCTTGTTTTAAACGATTTGCTGCAGTGTTTTTATAGTGGATTA  
ACAAAAACAGTACGGCGTTGCCTCGCCTTAGCTCAAGAGAACGATTCTCTAAGGTGCTGAAGCACCAAGTGAATCGGT  
TCCGTACTATCTGTACTGTCTGCGGCTTCGTGCGCTTGTCTGATTTTGTTAATCCACTATATAAGCGCAAAACAAATCG  
GCGGCCCGCGGAAAAACCCCCGAACGCGTCCGGAATATGCTTATCGATGGAACCGCAGCCGCATCCCCGCGCGG  
GCGTTTCAGACGGCACAGCCGCCCGGAAATGTCGACGCTTAAGGCACAGACGCACAAAAACCGTATGCTCGCAC  
45 CTGCAACAATCCGACAGATACCGTGTTTTTTCCAAACCGTTTGCAAGTTTCAACCATCCGCCGCGTGATGCCGCCACCA

CCATTTAAAGGCAACGCGCGGGTTAACGGCTTTGCCG

SEQ. ID NO:3

Nucleotide sequence of DNA region (1000 bp ) up-stream from the D15/Omp85 gene in the *Neisseria meningitidis* serogroup B strain ATCC13090.

5 ACCATTGCCGCCCCGCGCGCTTCCAAAGCGGCGACAAAATACAATCCGTCAACGGCACACCCGTTGCAGATTGGGGCAG  
CGCGCAAACCGAAATCGTCTCAACCTCGAAGCCGGCAAAGTCGCCGTCGGGTTGAGACGGCATCAGGCGCGCAAACCGT  
CCGACCATCGATGCCGACGGCAGCCCGGAAGCCGGTAAATCGCAAAAAACCAAGGCTACATCGGACTGATGCCCTTTA  
10 AAATCACAACCGTTGCCGCTGGCGTGGAAAAAGGCAGCCCCGCCGAAAAAGCAGGCCTGAAACCGGGCGACAGGCTGACT  
GCCGCCGACGGCAAACCCATTACCTCATGGCAAGAATGGGCAAACTGACCCGCCAAAGCCCCGGCAAAAAATCACCCCT  
GAACTACGAACGCGCCGGACAAACCCATACCGCCGACATCCGCCCGGATCTGTGCAACAGCCCGACACACCCCTGATCG  
GGCGCGTCCGCCTCCGTCCGACGCGGACAGGCGTGGGACGCGCAAATCCGCCGCGAGTACCGTCCGTCTGTTATCCGC  
GCATTCCGGCATGGGCTGGGAAAAAACCGTTTCCCACTCGTGGACAACCTCAAATTTTTCGGCAAACTAATCAGCGGCAA  
CGCCTCCGTACGCATATTTCCGGGCGCTGACCAATTGCCGACATTGCCGACAGTCCGCCGAACCTCGGCTTGCAAAGTT  
15 ATTTGGAATTTTGGCACTGGTCAGCATCAGCCTCGGCGTGTGAACCTGCTGCCCGTCCCCGTTTTGGACGGCGGCCAC  
CTCGTGTTTTATACTGCCGAATGGATACGCGGCAAACCTTTGGGGCAACGCGTCCAAAACATCGGTTTGCGCTTCGGGCT  
TGCCCTCATGATGTGATGATGCGGCTCGCCTTCTTCAACGACGTTACCCGGCTGCTCGGTTAGATTTTACGTTTCGGAA  
TGCCGTCTGAAACCGCATTCGCGACCAACAAGGAACTGACA

20 SEQ. ID NO:4

Nucleotide sequence of DNA region (1000 bp ) up-stream from the Hsf-like gene from *Neisseria meningitidis*

25 ATTCCCGCGCAGGCGGGAATCCAGAAACGCAACAGGAATTTATCGGAAAAACAGAAACCTCACCGCCGTCATT  
CCGCAAAAGCGGGAATCTAGAAACACAACGCGGCAGGACTTTATCAGAAAAACAGAAACCCACCGCCGTCATTCCCGC  
AAAAGCGGGAATCCAGACCCGTCGGCAGCGGAACTTACCGGATAAAACAGTTTCTTAGATTCCACGTCCTAGATTCCCG  
CTTTCGCGGGAATGACGAGATTTTAGATTATGGGAATTTATCAGGAATGATTGAATCCATAGAAAAACACAGGAATCTA  
TCAGAAAAACAGAAACCCACCGCGTCATTCCCGCGCAGGCGGGAATCCAGAAACACAACGCGGCAGGACTTTATCGG  
AAAAAACCGAAACCCACCGACCGTCATTCCCGCAAAAGTTGGAATCCAAAACGCAACGCAACAGGAATTTATCGGAAA  
AAACAGAAACCCACCGCGTCATTCCCGCGCAGGCGGGAATCCAGAAACACAACGCAACAGGAATTTATCGGAAAAAC  
30 AGAAACCCACCGACCGTCATTCCCGCAAAAGCGGGAATCCAGCAACCGAAACACAGGAATCTATCAGCAAAACAG  
AAACCCACCGACCGTCATTCCCGCGCAGGCGGGAATCCAGAAACACAACGCGGCAGGACTTTATCGGAAAAACAGAA  
ACCCACCGACCGTCATTCCCGCAAAAGCTGGAATCCAAAACGCAACGCAACAGGAATTTATCGGAAAAACAGAAAC  
ACCCACCGACCGTCATTCCCGCAAAAGCGGGAATCCAGACCCGTCGGCAGCGGAACTTACCGGATAAAACAGTTTCTTAGAT  
CCACCGCGTCATTCCCGCAAAAGCGGGAATCCAGACCCGTCGGCAGCGGAACTTACCGGATAAAACAGTTTCTTAGAT  
35 TCCACGTCCAGATTCCCGCCTTCGCGGGAATGACGAGATTTAAGTTGGGGGAATTTATCAGAAACCCCAACCCCA  
AAACCGGGCGGATGCCGACCATCCGCCCAAAACCCGATTTAACCATTCAAACAAACCAAGAAAAACAAA

SEQ. ID NO:5

Nucleotide sequence of DNA region (772 bp ) up-stream from the PilQ gene from *Neisseria meningitidis*

40 GCGATGTCGGGAAGCCTTCTCCGAATCATTACCCCTTGAGTCGCTGAAAATCGCCCAATCTCCGGAACAGGCGGCAAT  
CATGACGGCAAGAGCAGCATCCTGAACCTCAGTGCCATTGCCACCACCTACCAAGCAAAATCCGTAGAAGAGCTTGCCGC  
AGAAGCGGCACAAAATGCCGAGCAAAATAACTTACGTTAGGGAAACCATGAAACACTATGCCTTACTCATCAGCTTTCT  
GGCTCTCTCCGCGTGTTCCTCAAGGTTCTGAGGACCTAAACGAATGGATGGCACAACCGCAGCGGAAGCAAAAGCAGAAA  
TCATACCTTTCCAAGACCTACCTTGCCGGTTGCGCCGGTATACAGCCCGCCGAGCTTACAGGGCCGAACGCATTTCGAC  
45 TTCCCGCGCATGGAACCGACAAAAAGGGGAAATGCCCCGACACCAAGCGTATTAAAGAAACGCTGGAAAAATTCAG  
TTTGGAATAATATGCGTTATGTCGGCATTGTAAGTCTGGACAGAAAGTCTCCGCTTCATCGAGGCTGAAGGTTATGTCT  
ACACTGTCGGTGTGCGCAACTATTTGGGACAAACTACGGTAGAATCGAAAGCATTACCGACGACAGCATCGTCTGAAC  
GAGCTGATAGAAGACAGCAGGGCAACTGGGTTTCCCGTAAAGCAGAACTGCTGTTGAATTTCTCCGACAAAAACCCGA  
ACAAGCGGCAGCACCTGCCGAGAACAAATTAAGAAGAGGATTACTCCATT

50

SEQ. ID NO:6

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the Hap gene from *Neisseria meningitidis***

GTGCGGCAAAAAACAGCAAAAGCCCGCTGTCGATTGCCTGACCGTCCGCGTCCGTAAAATCAGCATAGGTTGCCACGCGC  
 GGCTTGGGCGTTTTCCACACAAAGCCTCTGCCATCGGAGCAGGTTTTTCCCGATATGCGTATCAGCCCACGCGCGC  
 5 GCGCCCGGGTGCGGTAGCGACTGCCGAATCGTTGGAACGTTATCCGACATAAAACCCCGAAATTCAAAACAGCGCGG  
 ATTATAGCAATGCCGTCTGAAGTCCGACGGTTTGGCTTTTCAGACGGCATAAAACCGCAAAATGCTTGATAAATCCGTC  
 CGCTGACCTAATATAACCATATGAAAAACGAACACATACGCCCTTCTGCTCGGTATAGGCTCGCTGCTGGGTCTGTT  
 CCATCCCGCAAAAACCGCCATCCGCCCAATCCGCCGACGATCTCAAAACATCGGCGGCGGATTTTCAACGCGCCATAG  
 AGAAAGCGCAAAATGACCGAAAAACGCACAGGACAAGGCGCGGAGGCTGTCGAAACCGTCGTAATCCCGGAGCTTG  
 10 TCGAGCAATCCTGTCGACGAGTACGTGCAAAATATGATAGCCCGGCTTTCCATTCCGGATCGTTGCCGCCCGCGTCCG  
 GACTTGGCGCAATACACGACATTATCAGCAACGGGCGAGACCGCATTATGGCAATGGCGGAAAAAGAACACCGTCCG  
 GCACGAAACCATACGGCAAGACCAACCTTCAACAGGCGCGGGCAACTGTACGGCTTCATCAGCGTCATCTGATACTGC  
 TTTTGGCGTCTTCTCGTATGGAGCGGCTACCCCGCAACCGCGCTCCCTTGGCGGCGCACAGTGGTTGCTTGGCG  
 GGTGCTTTCGTGATTGGAAGAAGCCGAGACCAAGCAAAATTAATTGCAATCCTAGGCGGTGCTTCATATCCGCCGGA  
 15 ACGCCGAACCGCACATATAGGCACATCCCGCGCGCGCGGGAAGCGGAGCGCGCTCCCAACAAACCCGAATCCCG  
 TCAGATAAGGAAAAATA

SEQ. ID NO:7

**Nucleotide sequence of DNA region (924 bp) up-stream from the NspA gene from *Neisseria meningitidis* (serogroup B) (ATCC13090)**

GGAAACGAACACGCGCTTCGGTCATACGCCGCCGAAAGGTTTGGCGCAAGACGAAGCCGCCCTCGACATCGAAGACGCGG  
 TACACGGCGCGCTGGAAGCGCGGGTTTTGTCCACTACGAAACATCGGCTTTTGGCAACAGCCATGCAGTCCCGCCAC  
 AATTTGAACCTACTGGCAGTTTCGGCGATTATTTAGGCATAGGCGCGGCGCTCACGGCAAAATTTCTATCCCGACCGCAT  
 20 CGAGCGCACCGTCCGCGCGCGCCACCCCAACGACTACCTCGCTTAATGCAAGCCCAACCGAGTGAAGCCGTGGAACGCA  
 AAACCGTTGCCGCGGAAGATTGCGGTTTGAAGTTCATGATGAACGCCCTGCGCTGACCGACGCGTACCCGCCCGCATGT  
 TCGAGAGCGCACGGGCTACCGAGTGCCTAAATCATGGCGCAATCGAAACGGCAAGGCAAAAGGCGCTGCTGGAACCC  
 25 GACCCCGCGCTATTCCGCGCGACCGAAAAAGGACGCTTGTTTTAAACGATTGCTGCACTGTTTTTATAGTGGATTAA  
 CAAAACCAAGTACGGCGTTGCTCGCTTAGCTCAAGAGAACGATTCTCTAAGGTGCTGAAGCACCAAGTGAATCGGTT  
 CCGTACTATTGTACTGTCTGCGGCTTCGTGCGCTTGTCTGATTGTTTGTAACTCACTATATAAGCGCAAAACAAATCGG  
 30 CGGCGCGCGGGAACCCCGCCGAAACGCGTCCGGAATATGCTTATCGATGGAACGACGCGCATCCCGCGCGG  
 GCGTTTCAGACGGCACAGCCGCGCGGAATGTCGACGCTTAAGGCACAGACGCACAAAAACCGTATGCTGCACCT  
 GCAACAATCCGACAGATACCGCTGTTTTTCCAAACCGTTTGCA

SEQ. ID NO:8

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the FrpB gene from *Neisseria meningitidis* (serogroup B)**

AAGTGGGAATCTAAAAATGAAAAGCAACAGGAATTTATCGGAATGACCGAACTGAACGGACTGGATTCCCGCTTTTCGC  
 GGGAAATGACGGCGCAGGGTTGCTGTTATAGTGGATGAACAAAAACAGTACGTGCTTGCTCGCTTAGCTCAAGAGA  
 ACGATTCTCTAAGGTGCTGAAGCACAAGTGAATCGGTTCCGTCTATTGTACTGCTGCGGCTTCGTGCGCTTGTCT  
 40 GATTTCTGTTTCGTTTTTCGGTTATTCCCGATAAATTACCGCGTTCCTCGTCATTTCCTTAACCTTCGTATTCGCGC  
 AGGCGGGAATCTAGTTTTTTGAGTCCAGTTGTTCTGATAAATCTTGACAGCTTTGAGTTCCTAGATTCCCACTTCG  
 TGGGAATGACGGTGGAAAGTTGCGGTGATTTTCGGATAAATTTTCGTAACGCATAATTTCCGTTTTACCCGATAAATGCC  
 CGCAATCTCAAATCCCGTCAATCCCAAAAAACAAAAACAGAAATATCGTCATTCCCGCGCAGGCGGGAATCT  
 45 AGACCTTAGAACACAGCAATATTCAAAGATTATCTGAAGTCCGAGATTCTAGATTCCCACTTTCTGTTGGGAATGACGAA  
 TTTTAGGTTTTCTGTTTTGTTTTCTGTCTTTCGCGGAATGATGAATTTTAAGTTTTAGGAATTTATCGGAAAAACAG  
 AAACCGCTCCGCGCTCATTCCCGCACAGGCTTCGTCAATCCCGCGCAGGCTTCGTCAATCCCGCATTTGTTAATCCACTA  
 TATCCCGCGCTTTTTTACATTTCGACAAAACCTGTCAACAAAAACACACTTCGCAAAATAAAACGATAATCAGCTT  
 50 TGCAAAATCCCCCCCCCTGTTAATATAAATAAAATAAATAAATAATTTTCTTATCTGCAAAATCTTAACGGT  
 TTGGATTACTTCCCTTCATACACTCAAGAGGACGATTGA

SEQ. ID NO:9

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the FrpA gene from *Neisseria meningitidis* (serogroup B)**

CTATAAAGATGTAATAAAAAATCTCGGTAACGGTAACACTTTGGCTCAGCAAGGCAGCTACACCAAAACAGACGGTACAA  
 CCGCAAAAAATGGGGGATTTACTTTTAGCAGCCGACAACTCTGCACAGCCGCTTCACGAACAAATGCTATCCATTAGCCAT  
 GTTCGGGAAAAACAGATTTCCCGTTTGTGTTTAGGCTGTCTAAACAAATAACCATAAATGTATATCATTATTTAAATAA  
 55 ATAAAAGTATTTAAGTATTATGACGAATTTTAGAGAAAGAGTAGACTGTGCGATTAAATGACAAACAAATAGTGAGAAAG  
 GAAATATTTACTATCCGAGCACAGCATATTTAGGTAGCCTGTAAGTGTTCCTGCTGGCGGAAGAGGATGAAGTTGGA  
 60 CTTACCCGAGAAATAATGTCCTGTTGTGTGATATGGATGCCATGCCGGAAGCAATTGATGCAATCAGGCGAGTCCCTACT  
 TGAATGAAACCTGTGCTTGCAGAAATTTGAAACGCTATTTTAAAGAAAGGATAAAGGAGAAAGATTTTGGTTTTTAA  
 GCTGCATGAAACCGTGTGGAATAAATGCACACCTACGATAAATAAATTTTCGTTTTTATTCTACAAGCTATTATATA  
 TATGATTGCTAAAGTTTTATTTTATAGTGCCAAAAAATATATTTATATACCTTCATATTGTTTATATGCTTTATTTGA  
 65 ATATATCTACGATGGGGAATATTTATATATTTTATAATAAATTTTACTCATTGCTAATATGTCATGGAATATTACTT  
 GTATTTTGTAGAATTTTTCATATGAAATATTCCATTACTATTTTCTGAACTTTATTAGTTTTTAAATATTTT

ACCTCTTATATTTACCATAAGAGAGCTAATTGATTATATTATATTGAGTCGATAATTAATTTATTCTTAATTTTAATTC  
CTCACGTTATTTTTTAAATTTACTTGAAAGGAAAGCAGAT

SEQ. ID NO:10

- 5 Nucleotide sequence of DNA region (1000 bp ) up-stream from the FrpC gene  
from *Neisseria meningitidis* (serogroup B)

GGAAACAGAGAAAAAGTTTCTCTTCTATCTTGGATAAATATATTTACCCCTCAGTTTAGTTAAGTATTGGAATTTATACC  
TAAGTAGTAAAAAGTTTAGTAAATATTTTTTAACTAAAGAGTTAGTATCTACCATAATATATTTCTTAACTAATTTCTAGGC  
TTGAAATATGAGACCATATGCTACTACCATTATCAACTTTTTATTTTGTATTATTGGGAGTGTCTTACTATGACCTCA  
10 TGTGAACCTGTGAATGAAAAGACAGATCAAAAAGCAGTAAGTGCACAACAGGCTAAAGAACAAACAGTTTCAACAATCC  
CGAGCCAATGACAGGATTTGAACATACGGTTACATTTGATTTTCAGGGCACCAAAATGGTTATCCCTATGGCTATCTTG  
CACGGTATACGCAAGACAATGCCACAAAATGGCTTTCCGACACGCCCGGGCAGGATGCTTACTCCATTAATTTGATAGAG  
ATTAGCGTCTATTACAAAAAACCCGACCAAGGCTGGGTCTTGTAGCCATACAACCAGCAAAACAAAGCACACTTTATCCA  
15 ATTTCTACGCGACGGTTTGGATAGCGTGGACGATATTGTTATCCGAAAAGATGCGGTAGTTTAAAGTACGACTATGGGAG  
AAAGATTGCTTACTTACGGGGTTAAAAAATGCCATCTGCCATCTCTGAATACGAGGCTTATGAAGATAAAAGACATATT  
CCTGAAATCCATATTTTTCATGAATTTTACTATATTTAAAAAGGAGAAAAATCCGGCGATTATTACTCATCGGAATAATCG  
AATAAACCAACTGAAGAAGATAGTTATAGCACTAGCGTAGGTTCTGTATTAAACGGTTTCACGGTACAGTATTACCCGT  
TTATTCGGGAAAGCAGCAGCTCACACAGCAGGAGTTGGTAGGTTATCACCAACAGTAGAGCAATTGGTACAGAGTTT  
20 GTAAACAAATTCAAATAAAAAATAATTTAAAGGATCTTATT

SEQ. ID NO:11

- Nucleotide sequence of DNA region (1000 bp ) up-stream from the Omp85 gene  
from *Neisseria meningitidis* (serogroup B)

ACGTCCGAACCGTGATTCCGCAACGCCGCGCCCAAAACCAAGCCCAAGCCAAAATGCCGATATAGTTGGCATTGGCAAT  
25 CGCGTTAATCGGGTTGGCGACCAAGTTTCATCAGCAGCGATTTCACACTTCCCAATGCCGGAAGGCGCGCGCGGACA  
CATCGCCCGCGCCGCCCAAAACAATGTGCGTGGGAAACCATACCGGCGATGACGGCGGTGAGGGTGCAGGAAACGTA  
CCAAATGAGGTAAGGATGATAATCGGCCTGATATGCGCCTTGTGCTTTTGGTGCTGCGCGATTGTGGCCGCCACCAA  
AATAAATACCAAAACCGCGCGACCGCTTTGAGCGCGCGGACAAACAGGCTGCCGAACAAGCCTGCCGCCAAGCCAGTT  
30 CGGGGAAACCGAACCATTACGATGCCAACGCCAAACCGCGGCAATCTGCCCTGACCAAGGCTGACGCGCGCCGATCGCA  
TGAATTAAGGATTGCGCAACGCCATAATCTTCCCTATGTTGTGATATGTTAAAAATGTTGATTTTAAAGAAAACT  
CATTCTCTGTGTTTTTTTTTATTTTTCGGCTGTGTTTAAAGGTTGCGTTGATTGCCCCATGCAAGTCCGGACAGGCTTTG  
CTTTATCATTCCGGCGCAACGGTTTAAATTTATTGAACGAAATAAATTTATTTAATCCTGCCATTTTCCGGCACTATTC  
35 GAAACCGCAGCTGTTTTCCATATGCGGATTGGAACAAATACCTTAAACAGCAGATACATTTCCGGCGGGCGCAAC  
CTCCGAAATACCGGCGCGCAGTATGCCGTCTGAAGTGTCCGCGCCGTCGGAACAACACAAAAACAGCCGTTTCAAAACCT  
GTCCGAACAGTGTTAGAATCGAAATCTGCCACACCGATGCACGACACCCGTACCATGATGATCAAAACCGCCCTGCT  
CCTGCCGGCTTTATTTTCTTCCGACGCATACGCGCT

SEQ. ID NO:12

- Nucleotide sequence of DNA region (772 bp ) up-stream from the PilQ gene from  
40 *Neisseria meningitidis* (serogroup B) (ATCC13090)

GCGATGTCGGGAAGCCTTCTCCGAATCATTACCCCTTGAGTCGCTGAAAATCGCCCAATCTCCGAAAACGGCGGCAAT  
CATGACGGCAAGAGCAGCATCTGAACCTCAGTGCCATTGCCACCACCTACCAAGCAAAATCCGTAGAAGAGCTTGCCGC  
AGAAGCGGCACAAAATGCCGAGCAAAATACTACGTTAGGGAACCATGAACACTATGCCCTACTCATCAGCTTTCT  
45 GGCTCTCTCCCGGTGTTCCCAAGGTTCTGAGGACCTAAACGAATGGATGGCACAAACGCGACGCCGAAGCCAAAGCAGAAA  
TCATACCTTTCCAAGCACTACCTGCGCGTTGCGCGGTATACAGCCCGCCGAGCTTACAGGGCCGAACGCATTCCGAC  
TTCCGCCGATGGAACCGACAAAAAGGGGAAATGCCCGGACACCAAGCGTATTAAAGAAACGCTGGAAAAATTCAG  
TTTGGAAATATGCGTTATGTCGGCATTGTTGAAGTCTGGACAGAAAGTCTCCGGCTTATCGAGGCTGAAGGTTATGTCT  
ACACTGTGCGGTGTCGGCAACTATTTGGGACAAACTACGGTAGAATCGAAAGCATTACCGACGACAGCATCGTCTGAAC  
50 GAGCTGATAGAAGACAGCACGGGCACTGGGTTTCCCGTAAAGCAGAACTGCTGTTGAATCTTCCGACAAAAACACCGA  
ACAAGCGGCAGCACCTGCCGACAGCAAAATTAAGAAGAGGATTACTCCATT

SEQ. ID NO:13

- Nucleotide sequence of DNA region (1000 bp ) up-stream from the Hsf-like gene  
from *Neisseria meningitidis* (serogroup B)

TTTGTTTTTCTTTGGTTTGTGTAATGGTTAAATCGGGGTTTGGGGCGGATGGTGCGGCATCCGCCCGGTTTTTGGG  
55 GGTGGGGGTTTTCTGATAAATCCCCCAACTTAAATCTCGTCATTCCCGCGAAGGCGGGAACTCTGGGACGTGGAATCT  
AAGGAAACTGTTTTATCCGGTAAGTTCCGTGCCGACGGGTCTGGATTCCCGCTTTTGCGGGAATGACGGCGGTGGGGTT  
TCTGTTTTTTCCGATAAATCCTGTTGCGTTGCGTTTTTGGATTCCAGCTTTTGCGGGAATGACGGTCCGTTGGGTTTTCT  
60 GTTTTTCCGATAAAGTCTGCCGCGTTGTGTTCTGGATTCCCGCTGCCGCGGAATGACGGTCCGTTGGGGTTTTCTGT  
TTTTGCTGATAGATTCTGTGGTTTTTCGGTTGCTGGATTCCCGCTTTTGCGGGAATGACGGTCCGTTGGGGTTTTCTGTTT  
TTCCGATAAATCCTGTTGCGTTGCGTTTTGATTCCCGCTGCCGCGGAATGACGGTCCGTTGGGGTTTTCTGTTTTTCCG  
CGATAAATCCTGTTGCGTTGCGTTTTTGGATTCCAATTTTGCGGGAATGACGGTCCGTTGGGGTTTTCTGTTTTTCCGA  
TAAAGTCTGCCGCGTTGTGTTCTGGATTCCCGCTGCCGCGGAATGACGGTGGGGTTTTCTGTTTTTCTGATAGA  
75 TTCCGTGGTTTTTCTATGGATTCAATCATTCTGATAAATCCATAATCTAAATCTCGTCATTCCCGCGAAAGCGGG  
AATCTAGGACGTGGAATCTAAGGAACTGTTTTATCCGGTAAGTTTCCGTGCCGACGGGTCTGGATTCCCGCTTTTCCGG  
GAATGACGGCGGTGGGGTTTTCTGTTTTTCTGATAAAGTCTGCCGCGTTGTGTTCTAGATTCCCGCTTTTGCGGGAAT  
GACGGCGGTGAGGTTCTGTTTTTCCGATAAATCCTGT

SEQ. ID NO:14

- Nucleotide sequence of DNA region (1000 bp ) up-stream from the Hap gene  
from *Neisseria meningitidis* (serogroup B)

AATCAGCATAGGTTGCCACGCGCGCTTGGGCGTTTTCCACACAAAGCCTCTGCCATCGGCAGCAGGTTTTTCCCGAT  
 ATGCGTATCAGCCCCACGCCCGCGCGCGGTGCGGTAGCGACTGCCGCAATCGTTGGAACGTTATCCGACATAAAACC  
 CCGAAAAATTCAAAAACAGCCGCGATTATAGCAATGCCGTCTGAAGTCCGACGGTTTGGCTTTCAGACGGCATAAACCG  
 CAAAAATGCTTGATAAATCCGTCCGCTGACCTAATATAACCATATGGAAAAACGAAACACATACGCCCTTCCTGCTCGGT  
 5 ATAGGCTCGTGTCTGGGTCTGTTCCATCCCGCAAAAACCGCCATCCGCCCCAATCCCGCCGACGATCTCAAAAACATCGG  
 CGGCGATTTTCAACGCGCCATAGAGAAAGCGCGAAATGACCGAAACGCACAGGACAAGGCGCGGACGCTGTGAAAC  
 CGTCGTCAAATCCCCGGAGCTTGTGAGCAAAATCCTGTCCGACGAGTACGTGCAAAATATGATAGCCCGGCGTTCCATT  
 CGGGATCGTGTCCGCGCGCTCCGACTTGGCGCAATACAACGACATTATCAGCAACGGGGCAGACCGCATTATGGCAATG  
 10 GCGGAAAAAGAACAGCCGTCCGGCAGCAAAACCATACGGCAAGACCAACCTTCAACAGGCGCGGGCAACTGTACGGCTT  
 CATCAGCGTCATCCTGATACTGCTTTTTGCGCTCTTCCTCGTATGGAGCGGCTACCCCGCAACCGCGCTCCCTTGGCG  
 GCGGCACAGTGGTTGCTTGGCGGTGCTTTCGTGATTGGAAGAAGCCGAGACCAAGGCAAAAATTAATTGCAAACTCTA  
 GGGCGTGCTTCATATCCGCCCGAACGCCGACATATAGGCACATCCCGCGCGCCGCGGAAGCGGAAGCCGCGCC  
 CTCCTCAACAAACCGGAATCCCGTCAGATAAGGAAAAATA

15 SEQ. ID NO:15  
 Nucleotide sequence of DNA region (1000 bp ) up-stream from the LbpA gene  
 from *Neisseria meningitidis* (serogroup B)

GATTTGGTTCATCCCGACAGCTTCTTGTGCAAGGGCGTGAAATTCCTTTGGTTAGCCAAGAGAAAAACCATCAAGCTTGC  
 CGATGGCAGGGAAATGACCGTCCGTGCTTGTGCGACTTTTGGACCTATGTGAAACTCGGACGGATAAAAACCGAACGCC  
 20 CGGCAAGTAAACCAAAGCGGAAGATAAAAGGGAGGATGAAGAGAGTGCAGGCGTTGGTAACGTCGAAGAAGCGGAAGGC  
 GAAGTTTCCGAAGATGAAGCGGAAGACCGGAAGAAATCGTCGAAGAAGAACCCGAAGAAGAGCTGAAGAGGAAGAAGC  
 TGAACCCAAAGAAGTTGAAGAAACCGAAGAAAAATCGCCGACAGAAGAAAGCGGCAGCGTTCAAACGCCATCTCGCTG  
 CCTCGGAAGCCTCTAAAGGCAGGACATCGACCTTTTCTGAAAGGTATCCGCACGGCGGAAGCCGACATTCCAAGAACC  
 25 GGAAAGACACATATACCGGCACTTGGGAAGCGGTATCGGCACACCCATTCAATGGGACAATCAGGCGGATGAAGAAGC  
 GGCAAAAGCAGAATTACCGTTAATTTCCGGCAGAAATCGATTTCGGAACGCTGACGGAGAAAAACGGGTGTACAACGCTG  
 CTTTCTATATTGAAAACGGCAAGATTGAGGGCAACGGTTTCCACGCAACAGCAGCAGCTCGTGAGAACGGCATCAATCTT  
 TCGGGAAATGGTTCGACCAACCCAGAACCTTCCAAGCTAGTGATCTTCGTGTAGAAGGAGGATTTTACGGCCCGCAGCG  
 GAGGAATTGGGCGGTATTATTTCAATAAGGATGGGAATCTCTTGGTATACTGAAGGTACTGAAAAATAAGTTGAAGT  
 30 TGAAGCTGAAGTTGAAGTTGAAGCTGAACTGGTGTGTCGACAGTTAGAACCTGATGAAGTTAAACCCCAATTTCGGCG  
 TGGTATTCGGTGCAGAAGAGATAATAAAGAGGTGGAATA

35 SEQ. ID NO:16  
 Nucleotide sequence of DNA region (1000 bp ) up-stream from the LbpB gene  
 from *Neisseria meningitidis* (serogroup A)

CGGCGTTAGAGTTTAGGGCAGTAAGGGCGCGTCCGCCCTTAGATCTGTAAGTTACGATTCCGTTAAATAACTTTTACTGA  
 CTTTGAAGTTTTTGGACCTAAGGGTGAAAGCACCCCTTACTGCTTAAAGTCCAACGCAAAAACCAAAAGACAAAAACACTT  
 40 TTATTACCCCTAAAATCGAACACCCATAAATGACCTTTTGTCTTTGGCGAGGCGCGCAGTAAGGGCGCGTCCGCCCTTAG  
 ATCTGTAAGTTATGATTCCGTTAAATAGCCTTTACTGACTTTGAGTTTTTTGACCTAAGGGCGGACGCGCCCTTACTGCT  
 TCACCTTCAATGGGCTTTGAAATTTGTTGCGCTTGGCTTGCTTGACCTAAGGGTGAAAGCACCCCTTACTGCGCCCTCGCC  
 45 AAAGACGAAAAGGGTTATTACGGGGGTGGATTTTAGGCGAGTAAGGGCGCGTCCGCCCTTAGATCTGTAAGTTATGATT  
 CCGTTAAATAGCCTTTACTGACTTTGAGTTTTTTGACCTAAGGGTGAAAGCACCCCTTACTGCTTCACTTCAATGGGCTT  
 TGAATTTTGTTCGCTTTGGCTTGCTTGAATCTAAGGGTGAAAGCACCCCTTACTGCGCTCTCGCCGAAGACAACGAGGGCTA  
 TTTACGGCGTTAGAGTTTAGGGCAGTAAGGGCGCGTCCGCCCTTAGATCCAGACAGTCACGCGCTTGAATAGTCCATTTT  
 50 GCCAAAGAATCTAAACGCGAGGACCTAAGGGTGAAAGCACCCCTTACTGCTTACATCCAAGCACCCCTTACTGCACCAG  
 TCCACGCACCCCTTACTGCCCTACGTCCACGCACCCCTTACTGCCCTACATCCAAGCACCCCTTACTGCTTACATAGACATG  
 ACAGACCGCGAGCAGCGGAACAGGACTAAAAACAATTAAGTGATATTTTGCCCACTATAATAGACATGTATAATTATA  
 TTACTATTAATAATAATTAGTTTATCCTCCTTTTCATCCC

55 SEQ. ID NO:17  
 Nucleotide sequence of DNA region (731 bp ) up-stream from the TbpA gene  
 from *Neisseria meningitidis* (serogroup B) (ATCC13090)

TATGAAGTCGAAGTCTGCTGTTCCACCTTCAATTATCTGAATTACGGAATGTTGACGCGC  
 AAAACAGCAAGTCCGCGATGCAGGCAGGAGAAAGCAGTAGTCAAGCTGATGCTAAAACG  
 60 GAACAAGTTGGCAAAAGTATGTTCTCCAAAGGCGAGCGCACCGATGAAAAGAGATTCCA  
 AACGACCAAAACCTCGTTTATCGGGGGTCTTGGTACGGGCATATTGCCAACGGCACAAGC  
 55 TGGAGCGGCAATGCTTCCGATAAAGAGGGCGGCAACAGGGCGGACTTTACTGTGAATTTT  
 GGTACGAAAAAATTAACGGCACGTTAACCGCTGACAAACAGGCAGGCGGCAACCTTTACC  
 ATTGTGGGCGTATTGAGGGCAACGGTTTTTCCGGTACGGCGAAAACTGCTGACTCAGGT  
 TTTGATCTCGATCAAAGCAATAACCCGCACGCTAAGGCATATATCACAACGCCAAG  
 60 GTGCAGGGCGGTTTTTACGGGCCCAAGCCGAAGAGTTGGGCGGATGGTTTGCCTATTCCG  
 GACGATAAAACAAACGAAAAATGCAACAGATGCATCCGGCAATGGAATTCAGCAAGCAGT  
 GCAACTGTGCTATTCCGTGCGAAACGCCAAAAGCCTGTGCAATAAGCACGGTTGCCGAAC  
 AATCAAGAATAAGGCCTCAGACGGCACCGCTCCTCCGATACCGCTGAAAGCGAAGAGT  
 65 AGGGAACACT

70 SEQ. ID NO:18  
 Nucleotide sequence of DNA region (373 bp) up-stream from the OmpA gene  
 from *Neisseria meningitidis* (serogroup B) (ATCC13090)

CGTACCGCATTCGCACTGCAGTGA AAAAGTATTGAAAGCAGTGAAGCAGGCGATAAAGTGC CGCACAAAGCGGTTTA  
 CCAAGAGTCCGTCAAAAGTCATCGACCGCATCGCCGACAAAGGCGGTTCATATAAAAACAAAGCGGCTCGCCACAAAACCC  
 75 GTTTGTCTCAAAAGTAAACCTTGGCTTGATTTTGC AAAACCTGCAATCCGGTTTTTCATCGTCGATTCCGAAAACCC  
 TGAAGCCCGACGGTTTTCGGGGTTTTCTGTATTGCGGGGACAAAATCCCGAAATGGCGGAAGGGTGC GGTTTTTTATCCG  
 AATCCGCTATAAAATGCCGCTGAAAACCAATATGCCGACAAATGGGGTGGAG

## SEQ. ID NO:19

**Nucleotide sequence of DNA region (1000 bp) up-stream from the *Pla1* gene from *Neisseria meningitidis* (serogroup B)**

5 TTTTGGCTTCCAGCGTTTCATTGTTTTCTGACAAAGTCGTAAGTCAGCTTCAGATTGTTGG  
CTTTTAAAGTCTTCGACCGTACTCTCATCAACATAGTTTCGACCGATTGTAGATGTTCA  
GAGTATCGGTGGCAGCGGCTTCGGCATTGGCAGCAGACGCGCTCTGCTTGAGGTTGCA  
CGGCGTTTTTTCGCTGCCGCGCAGGCTGCCAGAGACAGCGCGCCAAAACGGCTAATA  
CGGATTTTTTCATACGGGCAGATTCTCTGATGAAAGAGGTTGGAAAAAAGAAATCCCGCG  
10 GCCCCATCGTTACCCCGCGCAAGGTTTGGGCATTGTAAAGTAAATTTGTGCAAACTCAA  
AGCGATATTGGACTGATTTTCTTAAAAAATTATCTGTTTCCAAAAGGGGAGAAAAACGT  
CCGCCCGATTTTGCGGTTTTTTTGGCTGTGTCAGGGTGTCCGACGGCGGATAGAGAGAA  
AGGCTTGCATATAATGAAACCCCTTTAAAAATTGCGCGTTTACAGAATTTATTTTCTT  
CCAGGAGATTCCAATATGGCAACAGCGCACAAAGCAGCAACCGTCCCGCGCAGTCCGTC  
15 AAACAACGCGCCCAATGCTAGCCTGCGTACCGCATTTCCGACCGCAGTGAAAAAGTA  
TTGAAAGCAGTCGAAGCAGGCGATAAAGCTGCCGACAAGCGGTTTACCAAGAGTCCGTC  
AAAGTCATCGACCGCATCGCCGACAAGGGCGTGTCCACAAAAACAAAGCGGCACGCCAC  
AAAAGCCGCTCTGTCTGCAAAAGTAAAAGCCTTGGCTTGATTTTGTGCAAAACGCCAAGGC  
GGTTGATACGCGATAAGCGGAAACCTGAAGCCCGACGGTTTCGGGTTTTCTGTATTG  
20 CGGGGGCAAAATCCCGAAATGGCGAAAGGGTGCATTTTTATCCGAATCCGCTATAAA  
ATGCCGTTTGAAAACCAATATGCCGACAATGGGGGCGGAG

## SEQ. ID NO:20

**Nucleotide sequence of DNA region (1000 bp) up-stream from the *FhaB* gene from *Neisseria meningitidis* (serogroup B)**

25 TACGGAAATGCAAGCGGATCCAGAAGTTACAGCGTGCATTATTCGGTGCCCGTAAAAAATGGCTGTTTTCTTTAATC  
ACAAATGGACATCGTTACACGAAAGCAACCGAAGGCTATTCGTCATACGATTACACGCGCAACAAATATCAGAGCAGC  
CTGGCCCGCAGCGCATGCTTTGGCGTAACAGACTTCATAAACTTCAGTCGGAATGAAATTTATGGACACGCCAAACCTA  
TAAATACATCGACGATGCCGAATCGAAGTGCACGCGCGCTCTGCGAGCTGGGAAGCCGAATTCGCCACCGTGTCT  
30 ACCTCAACCGTTGGCAGTTGACGGCAAGTTGTCTTACAAACGCGGACCGCATGCGCCAAAGTATGCCTGCACCGGAA  
GAAAACGCGCGCATATTCTTCCAGGTACATCTCGTATGAAATCATTACTGCCGGTTTGACGCGAGCGCCCATTTAT  
TTTAGGCAACAGCAGTTTTCTACGCAACCGCCATTCAAGCTCAATGGAACAAACGCGGTTGGTTGCCCAAGATAAAT  
TGTCATTCGCGAGCCGCTACACCGTTCCGCGATTGTATGGGAGCAGAGTCTTTTCGGAGAGCGAGGTTCTACTGGCAG  
35 AATACCTTAACTTGGTATTTTCATCCGAACCATCAGTTCTATCTCGGTGCGGACTATGGCCGCGTATTGGCGAAAGTGC  
ACAATATGTATCGGGCAAGCAGCTGATGGGTGCAGTGGTCCGGCTTCAGAGGAGGGCATAAAGTAGGCGGTATGTTGCTT  
ATGATCTGTTTGGCGGCAAGCCGCTTATAAACCCAAAGGCTTTCAGACGACCAACACCGTTTACGGCTTCAACTGAAT  
TACAGTTTCTAACCTCTGAATTTTTTACTGATATTTAGACGGTCTTCTTATCTCAGACCGTCAAACTTACCTACGT  
ACTTGCGCGCAGTACGTTTCATCTTCAAAATGGAATAGAC

## SEQ. ID NO:21

**Nucleotide sequence of DNA region (1000 bp) up-stream from the *Lipo02* gene from *Neisseria meningitidis* (serogroup B)**

45 TTATCTTGGTGCAAACTTTGTGCGGGTCCGACTGGCTACGGCTTTGGGTTTGGACCCGCTCATCGGTCTGATTACCGGT  
TCGGTGTCTGCTGACGGGCGGACACGGTACGTACGGTGGTGGGACCTAATTTTGAACGCAATACGGCTTGGTCCGGCGC  
AACCCTTTGGGTATTGATCGGCTACTTTCCGGCTGGTGTTCGGCGGCTGATCGGCGGGCGGTTGCGCGCGCGCTGA  
TCAACAAAAATGGGCGCAAAACCGGTTGAAAACAAAAACAGGATCAGGACGACAACGCGGACGACGTGTTCCGACGGCA  
AAACGCAACCCGCTGATTACGGCGGAATCTGCCGTTGAAACGCTTGCATGTTTGGCCGCTGTTGGCGTTTGGCGAGAT  
TTGACAGCGCTTCGACAAAGAATATCTGTCGACCTGCCCAAATTCGTGTGGTGTCTGTTTGGCGGCGTGGTCATCCGCA  
50 ACATCTCTACTGCCGATTCAGGTCAATATGTTGCAACCGGCCATCGATGTGTTCCGCAATGCTTCGCTTTTCTGCTTTT  
TTGGCAATGGCGTTGCTGAATTTGAACTGTGGGAGCTGACCGGTTTGGCGGGCGCTGTAACCGTATCTTGGCGTACA  
AACCCTGGTATGTTTTGTACGCGACTTTTGTACCTATGTCTTTATGGGGCGGACTATGATCGGCGAGTATTGGCTG  
CCGGCCATTGCGGTTTTCGCTTGGGTGCAACGCCGACGGCGGTGGCAAAATATGAGTCCGTCACGCATATTTCCGGCGG  
TCGCATAAGGCGTTTTTGTATTGTCCTATGTTGCGCGCTTCTTCGTGATTTGATTAATGCGCGGATTCTGACCGGTTT  
55 TGTGAATTTCTTTAAAGGCTGATTTTCCGCCCTTCCGACAAAGCACCTGCAAGGTTTACCGCTGCGAGTGCTTTTGCTA  
TGATAGCCGCTATCGGTCTGCACCGTTTGAAGGAACATC

## SEQ. ID NO:22

**Nucleotide sequence of DNA region (1000 bp) up-stream from the *Tbp2* gene from *Neisseria meningitidis* (serogroup B)**

60 CCTACTCCACCGATTCCAATATGCTCGGCGGACCCAGCAAGCCAAAGACTTGAATTTTTGAACTCGGGCATCAAAATC  
GTCAAAACCATATGGGCGTTGCCTTTTGGGACGAAACGTTGAAGTCAGCCCCGAAGAGTCAGCGTGGCGTTTGAAGA  
AGGCGTGCCGTTGCTAGTGAACGGCAAGAATACGCCGACCCCGTCGAATCTTCTCGAAGCCAAACCGCATCGGCGGGC  
GCCACGGCTTGGGTATGAGCGACCAATTCGAAACCGCATCATCGAAGCCAAATCGCGCGGATCTACGAAGCCCGGGT  
65 ATGGCGTTGTTCCACATCGCTACGAACGCTTGGTACCGGCATCCACAACGAAGACACCATCGAACAATACCGCATCAA  
CGCCCTGCGCTCGGCCGTTTGTCTTACCAAGGCCGCTGGTTTCGACAGCAAGCCCTGATGTTGCGGCAACCGCCCAAC  
GCTGGGTGCGCAAGCCGTTACCGGCAAGTTACCTCGAACTGCGGCGCGGCAACGACTACTCGATTCTGAACACCGAA  
TCGCCCAACCTGACCTACCAACCCGAACGCTGAGTATGGAAGAGTCGAAGTGGCGGCTTACCCCGCTCGACCGCAT  
CGGACAGCTCAGATGCGCAACCTCGACATCACCGACCCGCGCCAACTGGGCATCTACTCGCAAGCGGTTTGTCTGT  
70 CGCTGGGCGCAAGGTCGTTATTCAGGAGTTGGCAATAAGAAATAAGGTTTGTCTTTTGCATCATTAGCAACTTAAGG  
GGTCGTCTGAAAGATGATCCCTTATGTTAAAAGGAATCCTATGAAAGATACAAAGTCGTCATTTATCAGGAAGCCAG  
TTGTCCAGCCTGTTTTTCCGGCGGGCAAGGTTCAACCCGCTCAATTTACGCGGTTCTTCAACAAACAAACCCCGGAAG

GCTGGCGGGTCGAGACCTTTGCAATAACATAGGTTACTAA

5 SEQ. ID NO:23

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the PorA gene from *Neisseria meningitidis* (serogroup B)**

GAATGACAATTGATAAGTTTCCCGAAATTCACATAACCGAAACCTGACAATAACCGTAGCAACTGAACCGTCATTCCCG  
 10 GCAAAAGCGGGAATCCAGTCCGTTCCAGTTTCGGTCATTTCGGATAAATGCCTGTTGCTTTTCATTTCTAGATTCCCACTT  
 TCGTGGGAATGACGGCGGAAGGGTTTTGGTTTTTCCGATAAATCTTGAGGCATTGAAATTCCAAATTCGCGCTGCGC  
 GGAATGACGGCTGCAGATGCCGACGGTCTTTATAGTGGATTAACAAAAATCAGGACAAGGCGACGAGCTGCAGACAGT  
 ACAGATAGTACGGAACCGATTCACTTAGTGCTTCAGTATCTTAGAGAATCGTTCTCTTTGAGCTAAGGCGAGGCAACGTC  
 GTACTGGTTTTTGTTCATCCACTATATATGACACGGAAACGCGCGCTCCAAACCATGCGCTCTGAGGAAACTACACA  
 15 GATACCGCGGTTATATTACAAATCGCGCCCGTGGTTCGAAACCTCCACACTAAAAAATAAGGAAACCCCTATGTCC  
 CGCAACACGAAGAGCTGCAAGGTATCTCGCTTTTGGGTAAATCAAAAACCCCAATATCCGCGCAATACGCGCCCGAAAT  
 TTTGGAAGCGTTCGACAACAAACATCCCGACAACGACTATTCGTCAAATTCGCTGCCCCAGAGTTCAACGAGCTCTGCG  
 CCATGACCGGGCAGCCGACTTCGCGCACCATCGTCATCCGCTACATTCCGCACATCAAAATGGTGGAAAGCAAAATCCCTG  
 AACTCTACCTCTTACGCTTCGCGCAACACGCGGATTTTCATGAAGACTGCGTCAACATCATCATGAAAGACCTCATTGC  
 20 CCGTATGGATCCGAAATACATCGAAGTATTGCGGAGTTCACACCGCGCGCGGCATCGCCATTTCATCTTTCCGCAATT  
 ACGGCAAGCAGGCACCGAGTTTGAAGCATTGGCGCGTAA

SEQ. ID NO:24

***Neisseria meningitidis* (serogroup B) PorA Promoter Region**

25 GATATCGAGGTTCGCGCTTGAATTGTGTGTAGAAACACAACGTTTTTGAAAAATAAGCTATTGTTTTATATCAAAATA  
 TAATCATTTTTAAATAAAGTTGCGGCATTTATCAGATATTTGTTCTGAAAAATGGTTTTTTCGGGGGGGGGTATA  
 ATTGAAGACGTATCGGGTGTGTCGCGATGTTTTTAGGTTTTATCAAAATTTACAAAGGAAGCCCAT

SEQ. ID NO:25

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the PorB gene from *Neisseria meningitidis* (serogroup A)**

30 gttttctgtttttgaggggaatgacgggatgtaggttcgtaagaatgacgggatataggtttccgtgcggtgaggttcgtc  
 attcccgcgagggcggaatctagaacgtggaatctaagaaacggttttatccgataagtttccgtgcggaacaagtttgg  
 attcccgccctgcgcggaatgacgggatatttaggtttctaattttggttttctgtttttgaggggaatgacgggatgtagg  
 ttcgtaggaatgacgggataggtttccgtgcggtgtaggttcgtcattcccgcgagggcggaatctagacctagaac  
 35 aacagcaatattcaaaagattatctgaaagtcgagattctagattcccgccctgagcggaatgacgaaaagtggcgga  
 tgacggttagcgttgcctcgccttagctcaaaagagaacgattctctaaggtgctgaagcacaagtgaaatcggttccgta  
 ctatttgcactgtctgcggttcgtcgccttgcctgatttttggtaatacactatctcctgcccgcagggcggttttg  
 catccgcccgttccgaaagaaacccggtgtgctgtttttgcccgtctttataacccccggtttgcaatgcccctcaatacc  
 ctcccgagtaagtggttgaataatgcaaatcttaaaaaatttaataaacatattgttataaaacaaaaatacccataat  
 40 attcttatccgtccttcaaaatgcacatcgaaattccacacaaaaacagggcagaagtttggtttttcagacaggaacatct  
 atagtttcagacatgtaatgcgcgagccctcggcggttaaatgcaaaagctaagcggttggaagccccggcgtgcttaaa  
 tttcttaacccaaaaaggaatacagcaatgaaaaatccctgattgcccgtgactttggcagcccttccctgttcagcaat  
 ggctgacgttaccctgtacggcaccatcaaaacccggcgta

45 SEQ. ID NO:26

***Neisseria meningitidis* (serogroup B) PorB Promoter Region**

50 GTTTTCTGTTTTTGAAGGAATGACGGGATGTAGGTTTCGTAAGAATGACGGGATATAGGTTTCCGTGCGGATGGATTCTGTC  
 ATTCGCGCGCAGGCGGGAATCTAGAACGTGGAATCTAAGAAACCGTTTTATCCGATAAGTTTCCGTGCGGGAAGTTTG  
 GATTCCCGCCTGCGCGGGAATGACGGGATTTAGGTTTCTAATTTTGGTTTTCTGTTTTTGAAGGAATGACGGGATGTAG  
 GTTCGTAGGAATGACGGGATATAGGTTTCCGTGCGGATGGATTCTGTCATTCCCGCGCAGGCGGGAATCCAGACCTTAGAA  
 CAACGCAATATTCAAAGATTATCTGAAAGTCCGAGATTCTAGATTCCCGCCTGAGCGGGAATGACGAAAAGTGGCGGGA  
 ATGACGGTTAGCGTTGCCTCGCCTTAGCTCAAAGAGAACGATTCTCTAAGGTGCTGAAGCACTAAGTGAATCGGTTCCGT  
 ACTATTTGTACTGTCTGCGGCTTCGTGCGCTTGCTCGATTGTTTGTAAATCCACTAT

55 SEQ. ID NO:27

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the siaABC gene from *Neisseria meningitidis* (serogroup B)**

60 ATACGGCCAATGGCTTCAGAAAGCGATAAGCCTCTGGCTGAAAAACCGATTCTTGTGTTCTCCCCACCGCACCCATAGA  
 CGTAAGGTATAGGATTTGGTAATCATGGTAACACATCACCGCGCAGCGAGCAAAATATTTTGTGCGGATTGCAACTA  
 AATCTTCAAGGCAACAGTTCGTACTACATTGCCACGTGTAGCTGCACATTCTGATCCTGCACATTTCGCGTTGAACCA  
 CCTACCGCAGCCACCGCATCCAACACACGCTCACCGGCTGCGGTCAGCGGCATACGCACACTATTCCGAGCACGAATCAC  
 CGACACATTGCGCGCATTTATCTGCACCAACGCAACCATCACTTGTGGCTGATTGGCCATTTTTTTCAGGCGGCCTTTAA  
 TAATTTCTGAACCTGACAGGCGTTTTACCGACCCGAAATATCGCCACAAACGGCACAGAAACCGTACCACTGCC  
 65 GTGACCAACTGCTCTGGCAACTTAGTTTGTATGCGCACTACCGAGGCCATCGAAGAAAGGCCACCACCAACCAATCTGC  
 CGCGCGCGCTTCCAAATCATAATATCAATACATCAACCAATATTAGCGTACCAGCCGAAGCATAAACATCGCCAACT  
 GAGTGAATGACTGATTTATCTGAGCCTTATATAAATGAGCAACCGATGATTACATCAATCAGCTCCACTTCAGGA  
 ATTTGAACCTCAGATTGTTGCCCTAAAGAGACAATTTTTTTCGCGTGGGCGCTGATGAAGGAATCGCAGAGCATCTAC  
 AATTAACCTCCACACAATAATACTGCGTGACGAATATAAAATTCACCTTTAAACACAAGCCAATCTAATATAAT  
 70 TATAAATGGCCTAATATAGCACTTAATCGAAATAAATTTATGAGTACGTAGAGTATAATTAGTATTCTTCTTCCAAC  
 TCCTTATACTTATATATATATCTTATAGATTCTAAATC

SEQ. ID NO:28



**Nucleotide sequence of DNA region (1000 bp ) up-stream from the lgt gene from *Neisseria meningitidis* (serogroup B)**

5 GCCAAAGCATTGGGCGCGGATGCCGCCGCTGCCGAACGCCGCCGCGCTCTTGCCAAAGCGGACTTGGTAACCGAAATGGT  
CGGCGAGTTCCCGGAAGTGAAGGACGATGGGCAATACTATGCTGTTTGGACGGCGAAACCGAAGAAATTGCCGAAG  
10 CCGTCGAGCAGCACTATCAGCCGCGTTTTCGCCGCGACAAGCTGCCGGAAGCAAAATTGCCGCCGCGCTGGCACTGGCC  
GACAACTAGAAACCTTGGTCGGCATTGGGGCATCGGTCTGATTCCGACCGCGGACAAGACCCCTACGCCCTGCGCCG  
CGCTGCCCTGGGTATTTGCGTATGCTGATGCAGTATGGTTGGACGTGAACGAACTGATTGACACGGCATTGACAGCT  
TCCCCAAAGTTTGTCTCAACGAAAAACGCCGCTCTGAAACCGCCGACTTTATGCAGGCGCGCTTGGCGTGTGGCTGCAA  
AAGCATTATCCGCAAGACATCGTTGCCGCCGCTACTCGCCAAACAGCCGCCGCTTGGACGATTGACCGCCAACTTGCA  
15 GGCCGTTGCCCGCTTCAAACAACCTGCCGAAGCCGCCGCGCTCGCCGCCGCAACAAACGCGTGCAAAACCTGTGAAAA  
AAGCCGATGCCGAGTTGGCGCGGTTAACGAAAGCCTGTTGCAACAGGACGAAGAAAAAGCCCTCTTTGCCGCCGCGCAA  
GGCTTGACGCCGAAAATCGCCGCCGCGCTCGCCGAAGGCAATTTCCAAACCGCCTTGTCCGAACTGGCTTCCGTCAAACC  
GCAAGTCGATGCATCTTTGACGGCGTGATGGTAATGGCGGAAGATGCCGCCGTAAAAACAAACCGCCTGAACCTGCTGA  
ACCGCTTGGCAGAGCAATGAACGCGGTAGCCGACATCGCGCTTTTGGGCGAGTAACCGTTGTACAGTCCAAATGCCGTC  
TGAAGCCTTCAGACGGCATCGTGCTATCGGGAGAATAAA

SEQ. ID NO:29

**Nucleotide sequence of DNA region (1000 bp) up-stream from the TbpB gene from *Neisseria meningitidis* (strain MC58)**

20 GAACGAACCGGATTCCCACTTTCTGTGGGAATGACGAATTTTCAAGTTACTGTTTTTGGTTTTCTGTTTTGTGAAAAATAA  
GGGATTTTCAAGTTTGTGGGTATTTACCGGAAAAACAGAAACCGCTCCGCCGCTATTCCCGCGCAGCGCGGAATCTAGGTC  
TGTCGGTGGGAACTTATCGGATAAAACGTTTCTTGGATTTTCTGCTCGGATTCCCACTTTCTGTGGGAATGACCGG  
AACAGAAACCGCTCCGCCGCTATTCCCGCGCAGCGGGGAATCTAGACATTCAATGCTAAGGCAATTTATCGGGAATGACT  
25 GAACTCAAAAACTGGATTCCCACTTTCTGTGGGAATGACGTGGTGACGTTTCCGATGGAATGGATTCTGCTATTCCCGC  
GCAAGCGGGAATCTAGACCTTCAATACTAAGGCAATTTATCGGAAATGACTGAACTCGAAAACTGGATTCCCACTTTT  
GTGGGAATGACGCGATTAGAGTTTCAAAATTTATCTAAATAGCTGAACTCAACACACTGGATTCCCGCCTGCCGCGGA  
ATGACGAAGTGGGAATTTACCGGAACTTAAACAAGCGAAACCGAAGCACTGGATTCCCACTTTCTGTGGGAATGACCGGA  
ATGTAGGTTCTGTGGGAATGACGCGGAGCGGTTTCTGCTTTTCCAAATAATGACCCCACTTAAATCCCGCTCATTTCC  
30 GCGCAGGCGGGAATCTAGGTCGTGCGTGCGGAACTTATCGGGTAAAACGGTTTCTTGAATTTTGGCTCTGGATTCC  
CACTTTCTGTGGGAATGACGGAATGTAGGTTCTGTGGGAATGACGGGATATAGGTTTCCGTGCGGACGCGTTCCGATTCTG  
ACTCGCGGGAATGACGGGATTTTGGTGATTCCCTAAAAAATAAAAAAGTATTGCAAAATTTGTTAAAAATAAATAAA  
ATAATAATCCTTATCATCTTTAATGAATTGGATTTATT

SEQ. ID NO:30

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the opc gene from *Neisseria meningitidis* (serogroup A)**

35 CAAAGGCTACGACAGTGGGAAAAACGGCAACATCTGGAAGAATCAGTTGTTGGACGGCATTATGCGCAAGCGCTGCC  
GCAACCGTCCGCTGTGCGGAAACGCAAAACCAACGCAACCGGTATTTGTCGAAGACCCGTTATAGTGGATTAAATTTAAAT  
CAGGACAAGGCGACGAAGCCGACAGACAGTACAAATAGTACGGCAAGGCGAGGCAACGCCGCTACTGGTTAAATTTAATCC  
40 ACTATATGTGTCGAACAGAGCTTCGCTACGCTGCACCGTAAATTTCCGCTATGCGCGGGCAGCCTATTTCGGACTGATTA  
AAGTAGGTTCTGTGGGAATGACGCGGATGTGTTTGAACCTGTTGAAAGCCGCCAACAAGCTAAGTCCGCCCTGCC  
GCCTAAAAGGAGACCGGATGCTGATTATCGGGTATCCGGGGAGGGTTAAGGGGGTATTTGGGTAAATTTAGGAGGTATT  
TGGGGCGAAAAATAGACGAAACCTGTGTTTGGGTTTCCGCTGTGCGGAGGGAAAGGAATTTTGCAAGATCTCATCTCT  
45 TATTTTCAAAAAACGAAAAACCAAAACAGCAACCTGAAATTCGTCATTCCCGCGCAGGCGGGAATCCAGAACCCCAAC  
GCGGCAGGAATCTATCGGAAATAACCGAAACCGGACGAACCTAGATTCCCGCTTTCCGCGGAATGACGGCAGAGTGGTTT  
CAGTTGCTCCCGATAAATGCCGCCATCTCAAGTCTCGTCATTCCCTTAAAAACAGAAACCGAAATCAGAAACCTAAAAAT  
TCGTCATTCCCTAAAAAACAGAAACCAAGTGAAGATAAATTCGTTGTAACAAATAACTATTGTTAATTTTATT  
AATATATGTAATATCCCCCCCCCCCCCGAAAGCTTAAGAAATATAATTGAAGCGTAACGATTATTTACGTTATGTT  
50 ACCATATCCGACTACAATCAAATTTTGGAGATTTAACT

SEQ. ID NO:31

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the siaD gene from *Neisseria meningitidis* (serogroup B)**

55 ATAATGCAGGCGCTGAAGTTGTTAAACATCAAACACACATCGTTGAAGACGAAATGTCTGATGAGGCCAAACAAGTCATT  
CCAGGCAATGCAGATGTCTCTATTTATGAAATTATGGAACGTTGCCGCCCTGAATGAAGAAGATGAGATTAAATTAAGA  
ATACGTAGAGAGTAAGGGTATGATTTTATCAGTACTCCTTTCTCTCGTGACGTGCTTTACGATTACACGATGGATA  
TTCCAGCATATAAATCGGCTCTGGCGAATGTAATAACTACCCATTAAATTAAGTGGTGGCCTCTTTTGGTAAGCCTATT  
ATTCTCTTACCGGCATGAATTTCTATTGAAGCATCAAAAGTCGGTAGAAATTATCGAGAAGCAGGGGTACCTTATGC  
60 TTTGCTTCACTGTACCAACATCTACCCAACCCCTTACGAAGATGTTTCGATTGGTGGTATGAACGATTATCTGAAGCCT  
TTCCAGACGCAATCATTGGCCTGTCTGACCATACCTTAGATAACTATGCTTGTCTAGGAGCAGTAGCTTTAGGCGGTTTCG  
ATTTTAGAGCGTCATTACTGACCGCATGGATCGCCAGGTCGGATATTGTATGCTCTATGAATCCGGATACCTTTTAA  
AGAGCTCAGCAAGGCGCTCATGCTTTAAATTTGGCACGCGCGGCAAAAAAGACACGATTATCGCGGGAGAAAAGCCAA  
CTAAAGATTTCCGCTTTGCATCTGTGCTAGCAGATAAAGACATTAATAAGGAGAACTGTTGTCCGGAGATAACCTATGG  
65 GTTAAACGCCAGGCAATGGAGACTTCAGCGTCAACGAATATGAACATTATTTGGTAAGGTCGCTGCTTGAATATTTC  
CAAAGTGCTCAAAATCAAAAAAAGTGAATTTAATTAAGCTTATTAAGTACTTTATTAACAGAGGATTGGCTATT  
ACATATAGCTAATTTCTCATTATTTTAAAGAGATACAATA

SEQ. ID NO:32

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the ctrA gene from *Neisseria meningitidis* (serogroup B)**

70 ATACCTGCACCTTGAAGTTGCCGACCAATAATTTAGCATGTTTCAATAAGACTAAAAATATTCAAATCGAATGGAAGGAAA

TGCAATAAAATTTATCAGATTGATATTTTAATAATCTTGCAGAATACTTTCAGTGCCAGTGTCATTATTAGGGTAGATGC  
 TAATGATATTTTGGCCACTTAATTCTAATGCTTTGAAATATTGGGCCGCATATTGTGGCATTAAATGTGCTTCTGTAGTC  
 ACGGGGTGAACATAGAAATACCATAATTTTCGTATGGTAAACCGTAATATTCTTTGACTTCTTCTAAGGATGGGAGGGT  
 5 GGAAGAGGGCCATAACATCTAAATCGGGGGAGCCGATGATGTGAATATGCTTTCTTTTCTCCCATTTGCAGTACGGCCGAG  
 TGACAGCTTTGTTTCAATTTGCTACCAAGTGGATATGAGAAAGTTTACTAATAGAATGACGAATGGAGTCATCTACTGTACCA  
 GATAGTTCACCACCTTCGATATGGCAAACCTAAACGGCTGCTTAATGCACCTACAGCTGCGCCTGCTAGTGCTTCTAAACG  
 GTCGCGGTGAATCATGACCATATCAGGTTCAATTTTCATCAGATAGACGAGAGATAAACGTAATGGTATTGCCTAAACGG  
 CACCCATTGGTTTCACTTTGGATTTGATTTGAAACAGATATGTATGTTGATAGTTTCTCGAGTTACTTCTTGTAGGTT  
 10 CTGCCATATGTTTTATCATATGCATACCAAGTTACAATCAAATGCAATTCAGGTCGCGGTGATTTTCAATATAGGCTAA  
 TAAAGGTTTTAGCTTGGCGAAGTCGGCTCTGGTACCTGTAATGCAAGAATCTTTTCATGATTTTAGAATCTATAAGTA  
 TATATATATAAGTATAAGGAAGTTGGAAAGAAGTAATAATTATACTCTACGTACTCATAAATTTATTTTCGATTAAAGT  
 CTATAATTAGGCCATTATATAATTATATTAGGATTGGCTT

SEQ. ID NO:33

15 **Nucleotide sequence of DNA region (1000 bp) up-stream from the lgtF gene from *Neisseria meningitidis* (serogroup A)**

TCTTTTTCGGACTGAAAGGACGCATCATCCCGACATCGAGCGGTGTCGTCGGCAGCCAAAGGCATAGGTTATGCCTAC  
 GAAGCCATCAAATACGGTCTGACCGATATGATGCTGGCGGGCGGAGGCGAAGAATTTTCCCGTCCGAAGTGATGTTTT  
 CGACTCGCTTTATGCCGCCAGCCGCGCAACGGCGAAGCGGAAAAACCCCGCGCCCATACGACGCGAACCAGCGGCGG  
 20 TGGTCATCGGCGAAGGCGCGGGGATTTTCGTGCTGGAAGAATTGGAACACGCCAAACGGCGCGGTGCGATAATTTACGCC  
 GAACCTCGTCGGCTACGGAGCCAACAGCGATGCCCTACCATATTTCCACGCCCCGCCCCGACGCGCAAGGCGCAATCCTTGC  
 CTTTCAGACGGCATTGCAACACGCGAGACCTTGCGCCGGAAGACATCGGCTGGATTAACTGTCACGGCACCAGGAGCGCACC  
 ACAACGACAGTATGGAAAGCGCGCCGTTGCAAGCGGTTTCGCGCAACAATACGCCCTGCAGTCCACCAAGCGCAAAAC  
 GGACACACGCTGGGGCGGGCGGGCAATCGAAGCCGCTTCGCGTGGGGCATTGCTGACCGGAAAGCAATCCCGAAGG  
 25 GAAACTTCCGCCAGCTTTGGGAGGGGAGAACGATCCCGACCTTCCCGCCATCAACCTGACCGGCAGCGGAGCCGCT  
 GGGAAACCGAAAAACGCATTGCGGCCAGCTCGTCGTTTGCCTTCGGAGGAAGCAACTGCGTTTTACTCATCGGATGAAAT  
 AAGTTTGTCAATCCACCGCTATGCTATACAATACGCGCTACTCTTGATGGGTCTGTAGCTCAGGGGTTAGAGCAGGGG  
 ACTCATAATCCCTTGGTCGTGGGTCGAGCCCCACCGGACCCACCAATTCCCAAGCCCGGACGTATGTTGGGCTTTTTT  
 30 GCGCCCTGTGAACCAAAATGCTTTGAGAAACCTTGATA

SEQ. ID NO:34

35 **Nucleotide sequence of DNA region (1000 bp) up-stream from the lgtB gene from *Neisseria meningitidis* (serogroup B)**

TAGAAAAATATTTCCGCCAATCATTAGCCGCGCTCGTGAATCAGACTTGGCGCAACTTGGAGATTTGATTGTCGATGAC  
 GGCTCGACAGACGGTTCGCTTGCCTTGCCTAAGGATTTCAAAGCGGGACAGCGGTATCAAATCCTTGCACAAGCTCA  
 AAATTCGGCGCTGATTCCCTCTTTAAACATCGGGCTGGACGAATTGGCAAAGTCAGGAATGGGGGAATATATGACGCA  
 CCGATGCCGACGATATTGCCGCCCGGACTGGATTGAGAAAAATCGTGGGCGAGATGGAAAAAGACCGCAGCATCATCGCG  
 40 ATGGCGCGCTGGCTGGAAGTTTGTGCGAAGAAAGGACGGCAACCGGCTGGCGCGGCATCACAGGCACGGCAAAATTTG  
 GAAAAAGCGACCCGGCAGGAATATTGCCGACTTTTTCCCTTTCGCGCAACCCCATACACAACAACACGATGATTATGA  
 GGCGCAGCGTCATTGACGGCGGTTTGCCTTACAACACCGAGCGGGATTGGGCGGAAGATTACCAATTTTGGTACGATGTC  
 AGCAAAATTTGGCAGGCTGGCTTATTATCCCGAAGCCTTGGTCAAATACCGCTTTCACGCCAATCAGGTTTCATCCAAATA  
 CAGCATCCGGCAACACGAAATCGCGCAAGGCATCCAAAAACCGCCAGAAACGATTTTTTCAGTCTATGGGTTTTAAAA  
 CCGGTTTCGACAGCCTTGAATACCGCCAAATAAAGCAGTAGCGTATGAATTGCTGGAGAAACATTTGCCGGAAGAAGAT  
 45 TTTGAACGCGCCCGCGGTTTTTGTACCAATGCTTCAAACGACGGACACGCTGCCCGCGCGCTGGCTGGATTTTGC  
 GGCAGACGGCAGGATGCGGGCGGCTTTTACCTTGAGGCAATACTTCGGCATTTTGCACCGATTGCTGAAAAACCGTTGAA  
 AACGCGCGCTTTATCCAACAGACAAAAAACAGGATAAAT

SEQ. ID NO:35

50 **Nucleotide sequence of DNA region (1000 bp) up-stream from the lgt gene from *Neisseria meningitidis* (serogroup B)**

GCGCACGGCTTTTCTTTCATCGGTTTGAAGGTGCGCAGGATAATCGGGGACGGCAAGCCTTTAGACTGCAATTTCTTTAA  
 TCGCGCGCGTCAGTTGAGGTACGGATGCGCTGATGTTGCGGAGTTTGATTACGTTTGCATCGGGCTGTTTACCAGTTTCG  
 CCAATTCGGCAAGCGCGTGGGTACGCGCTGCGCTTCGCTCAGATATTGCGGGAATGCGGCCAAAAATACGGCCGGACAG  
 55 GGAATGTGCGCAGTTTTCATCAATATCGGCGTGGCGGGCAACGCCTGCACAATCGGCAGCAGCGATTGGGTGCGCA  
 GCGCGGGGGCTTCGTCGGTATGGGTATAAACAATGGTGATTTTTCAGTCATAGGATTATCTCTTGTAGGTTGGTTTTT  
 TCTTTTGGAAACATTTGCGCGGGGAATGTGCGCGGCTATTATGGCATATTTTGGCGGCTTTGTTGCGCTTTGTTTCGATC  
 TTGGCGTGTTTGAACGCGGCGAGCGTGAAGGAAGGGGAAATGGTTTTCCCGCTTTGGCGGCGGTGTCGGAGGTGCTGT  
 GCCTGATGTGCGGCGGCATATTTTCGGTGAAATGATTTTATAGTGGTTTAAATTTAAACCACTACAGCGTTGCCTCGCC  
 60 TTGTCGTACTATCTGTACTGCTGCGGCTTCGTTGCTTGTGCTGATTTAAATTTAAACCACTATAATATTCCGTTAATC  
 TCGGAATATCTGCTAAAATTCGCAATTTTCCGCCCTCGGGACACTCGGGCGGTATGTTAATTTGTCGGAATGGAGTTT  
 AGGAT

SEQ. ID NO:36

65 **Nucleotide sequence of DNA region (1000 bp) up-stream from the msbB gene from *Neisseria meningitidis* (serogroup B)**

GCGGACGGCGAAGACAGACGTCGTGAATCAACCGCTTGGACAGTACGGCGGCGCAATACGACATGCTTGCAGGTTATC  
 TTGAAGACTTGCAGGAAACCGACCGTTGGCGTGGCGCTACCGCCAAATGCGGCTGTAACACCCGATATCTCTTTT  
 GAAAGCGGATATGCCCCATACCTTCCCGATATTTCCCAATGTATCAGACAAAATTTGGAACAATATTTCAAAGACCT  
 70 GAACGGTACCGAACCTTTCGCGGCTGTACGATATGGTCTGCATCAGGTGGAACAAACCGCTGCTGGTGTGCGTGTGAAC  
 AATCGGCGGCGCAACAGTCCAAAGCCTCCGTCATGTTGGGACTGAACCGCAATACTTTGCGTAAAAAATGATTCAACAC  
 GGTTTGCTGTAATGTGCGCAACCGTCCGTCATCTTTGGGTATGACCCGGGACGTGCGGTAAACGGGTTTCGGTGTGTCATC  
 GATGTGAGGGGCGGATCATTTTACGTCGCTCCGGCTGCATCAAAACGCGTCCCGATGCGCCTCTGGCAGACAGGAT  
 TGCGGTGATTGTGCGGCATATCGCGAAGTCGTTACCGTTTACAAGCCTCAACAGGCGGAGTGAACAGGTGTTCTGTC

ACGTCAATCCGGCATCGACGCTGATGCTCGGTGAGGCTAGGGGCGCGGCATTGGCGGCATGGTCAGCCATAAGCTGCCC  
 GTTTCGGGAATACAGGCCTTGACGGTCAAACAGGCGGTAGTCGGCAAGGGCAAGCGGCAAAAGAACAGGTGCAGCATAT  
 GGTGGTGCAGATGCTGGGGCTTTCGGGAACGCCGAGGANTGGCGCGGACGGTCTTGCCGTGCGCGTGACCCACGCCTT  
 ACGCAACCACGGGCTTGCCGCCAACTCAATCCTTCGGGGATGCAGGTCAAGCGCGCAGGTTTCAATAGTTTCAGACGG  
 CATTGTATTTTGCCGTCTGAAAAGAAAATGTATATCGAG

# SEQ. ID NO:37

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the htrB gene  
 from *Neisseria meningitidis* (serogroup B)**

CCGCCAAGCGTTTCCCCCTTTGTGCGGGCTTAACATTTGCTTTGTACGGCAGACTTTTCCCTTCATAACGCCGCTTTCC  
 GAAAAGACGATGGTAGGCGCGACGTAATTCTCAACCTTAAGGTACGGTTGGACGAAAAGTTTCCCTTTTATTCCACCT  
 GCCAATCTTTCGGGTACACCGAGTGGTCTCGTTAGGTTTGGGCGAACTACGCCCTTAAAAAACGGACATTCTTTCATG  
 CCCGTCTCTAAGGTTTCACGGTAAGTTTACCCTTATAAAGAGTTGACTTACCATACTTATCCCTTTAAACGATATAAAG  
 GCGACAGCTGTAATACAAGTATGTTGTACGGCAGACTTCTTACCAAAACAAAAGTTCCCTTTAGAGTTACTCGCTTA  
 TAGACAAATGAAGGCTTAGCCATAGGCTTCGGTAGGCTTATTCAACGGCTGGTTACAGGCTACGCTAAAACCTACGG  
 TAGAACCCGCTTCTGGGGTTTCGCGCACAGCGCGCTCTTTGGAACAGTTGTGTCGGAACACGCATAACCGCCCGCTTA  
 ATGCGGTGGCGGTTACCTGATGATTTTCAGCGTGGCTTGGTAGTTTGGCTAGCCGATGTTGAGGAGGCTCGACC  
 CGAACTACGGTTGCCAGCGCCAGCGCACATGATGCTGGTCTGTAGAGGCTGTAGCGGGTTCCGCACTTGCTTCGG  
 CTTCCGTAATGAACTTGGTTCCGCGACCGCTGGTTCCAAATACAAAGCGATACGGACGCTGCTTTGGGGCTGGGACTA  
 CGGCAACCGGTAGATAATGTCGGTGGCGGACTACGTCGAGTTTCGCTTAATGCGTTTCTGCCGAGGACGGAACCGACG  
 CAGGGCTCGCTTTTCGGGTGACTGGCACCATAATGCTATCGCTTAGGCCGTTTCATTTTGGCTAACTATGGCAGCAGGAG  
 AGATACGTTGTGCTGGGCCCTTAGCCAATACTTCTCACT

# SEQ. ID NO:38

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the MltA gene  
 from *Neisseria meningitidis* (serogroup B)**

CACAAAAACCAAGTTATGACGGGAATAAGGTACAGCAGCCAAACCAAGCGCTCGCCCTGC  
 GTCGGATGGTTCGGTATAGCCGAAAAATCCGCCGAGCAGCAGCCCAACGGCTGTCTTCG  
 TGCAATATTTTGTAGTGAACACAATGTCTGAAGCGCGTTCCAAATGCCTGCTTCG  
 TGACGCGCAGCAGCAACCGCAAGCAGACAGCGGCAACGATAATCAGAAACGCCCT  
 GTCCAAACGAAAACTTCGCCAGATTACGGCGCATCCACCTGATAAATCAACGCGCCA  
 ATCAGCGCGCAGCAAAACCCCGCTACCGCACCGCGCGCATCTGCCACGTGCGGCTC  
 TGTTTGAATACGGCAAGCAGGAAAAACGCTCTCCAAACCTTCGCGCGCCACGGCAAGA  
 AACCGCATACCGAACAGGCCCATCTCTTGACCGCTGCCACGGTTCAAAGCCGCTGCACA  
 GAATCTGAAGCTGCCGCTTCATCGAACGGGCGGCTTTTTTTCATCCATAAAATCATATAA  
 GTCAGCATCGCGACAGCAACCAACCGATAATGCCGACGACGAACTCCTGCTGCTTCTGG  
 GGAATCTCGCCGTTTCCGAATGGATTCCGTACCCAGCCCCAAACACATCAAAGAAGCA  
 AGAACCAACCCCGCTTAGGCATCAGTTTGAATGTCCGGACTGTTTCAGAAAA  
 CCGGCAACGATGCCGACGATGAGCGCGCTTCGATACCTCGCGCAACATAATTAAAAAA  
 GCGACCAGCATAAACGCGAACGAACAAGGATGATGAATAATATATATCGGAATATTTTC  
 ATTGCTTGTAATAACAATGCAAGTTATTTTTATCTGCAGTACCGCGCGGCGGAAAGTTC  
 CGCAGCTGCAGCTGCGCCCTGTGTTAAATCCCTCTCCACGGCTGCGCGCAACGCGGCC  
 GAAACCATCTTTCTTATTACTGCCGGCAACATGTCCATT

# SEQ. ID NO:39

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the ompCD gene  
 from *Moraxella catarrhalis***

GCTGATTTGTGAGCAAGCGGGCGCATCAGGGATTACCTTGCAATTTGCGAGAAGATCGTCG  
 ACATATTCAAGATGAAGATGTTTATGAATTGATTGGGCAATTGACAACACGCATGAATCT  
 TGAGATGGCAGTCACTGATGAGATGCTAAATATTGCCCTAAAGGTACGACCAGCATGGGT  
 GTGTTTAGTACCAGAAAAACGCCAAGAGCTGACTACAGAAGTGGGCTTGATATCGCCAA  
 TTTATCAAATATTCAAGCATTTATACACAGTCTTCAGCAGGCGGATATTAAAGTTTCTTT  
 ATTCATCGATCCAGATCCGCATCAAATTGATGCTGCAATTGCTTTGGGTGCTGATGCGAT  
 TGAGCTGCATACGGGAGCTTATGCTCAAGCGACTTTACAAAAATATCAAAAGCTTGTTGA  
 TAAAGAGCTTGACCGTATTCAAAAAGCCGTTGCAATGGCACAAAAAAATCATCATTATT  
 GATTAAATGCAAGTCATGGTTTACGCGTGATAATGTTGCAGCGATTGCCCAAATTGATGG  
 TATTCAAGCTGAAATATCGGGCATGCATTGATTTACAGATGCGATATTTATGGGCTTGA  
 TAATGAGTCAAGGCAATGAAAAATGGCTTTTATTCAAGATAAACGACCAATCATTGATG  
 CGTTAGAAAGAAAAATCGTAAATATGATGACTATTGTGAATATTATGATTTTTGTTCA  
 AAAAAAGGTTGTAAAAAAATTCATTACCATTAAGCTAAGCCCAAGCCACAATGAATA  
 CCTATTGGTTTACTCATTAGTCACTAAGAATCTGCAAAATTTGTAACAGATTATTGGC  
 AGGTCTTGATCGCTATGCTAAATAGGTGCGGTAATCTTGA AAAACCAACCATTCCTTG  
 GAGGAATTTATGAAAAAGGATATAAACGCTCTTGCGGTCACTCGACCGTTGACAGTCC  
 AGTTGCAGTCCAGTTGCTGCTCAAGCTGGTGTGACAGTC

# SEQ. ID NO:40

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the copB gene  
 from *Moraxella catarrhalis***

GATGCTGTTAAAGTGGGTATTGGTCTGTTCTATTTGTACAACCCGATTTGTTGCAGGC  
 ATTGGCGTCCCGCAGATAAGTGCCATTGATAGTGTGGCAAGTGCGTTAAAGATCGCATT

SEQ. ID NO:41

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the D15 gene from *Moraxella catarrhalis***

SEQ. ID NO:42

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the omplA gene from *Moraxella catarrhalis***

SEQ. ID NO:43  
Nucleotide sequence of DNA region (1000 bp ) up-stream from the hly3 gene  
from *Moraxella catarrhalis*

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AAATGGGTTAAACCTTGACATGATTGTTGACATGATTGACAGACAATAAAATTTGGCAAA  
TTTGATAAAATTGGTGATGTGTGTGATTTATCAAAAGCAGCTTGAATTAACCGAGTGTA  
TAGCGTAAATTTGTAGCAAAACCAATCAATTCATCATATAATTTAATGAACACGAGGTTAAAT  
TACTACTGATTTGTCTGATGACAAATTCAGCACTTGGTTCG

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SEO. ID NO:44

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the lbpA gene from *Moraxella catarrhalis***

TAACAAAGGCAACCCAAACGCGAGTTATTTTGTGCAAGGCGGTCAAGCGGATGTCAGTAC  
TCAGCTGCCGATCGCAGGTAATTCACCTATATAGTCTTTGGGCAAGGCTACCTGCACCA  
GAAAAAGCAAAAGGTTATGACCAAGATGAGGATACCATCAAGCAAAAAGGCTCTAAAGA  
TTATATATTGACCAAGACTTTATCCCACAAGATGACGATGACGATGACGATGACGATG  
TTTGACCGCATCTGATGATTCACAGAATGATATACACATGGCGATGATGATTTGATGTC  
ATCTGATCTTCAAGAATGATGACGCGATGGCGATGACGATTCAGATGATTTGGGTGA  
TGGTCGAGATGATGACGCCGAGGCAAAAGTGATCATGCGGTAATATCTCGCCCTGAT  
TGAAACAACAACTTGCCTAATTAAGGCTACTCTAGTAAACAACTTTGCCCTAGATTG  
TAAAAATAAGGCTAAGTTTGTATGTAACTTTGACACCAACGCCTAAGTGGTAAATTA  
CGATGAGACGAGGTGATCTGCTTTGATATCAAAATGGCAAAATGATGGCAGAGGAT  
TACCGCCAAAGCGGATGTGCCAACTCTGTAAGAAGTGGGTAACAAACCAAGGTGGCGG  
TTCTTTACAACATCAAGAAATTTGATGTTAAGGGGCAATTTTGGCACAATGGCGCA  
AGAGTTGGCAGACGGTTACATCATCAAGAGCGGATGGCATCTGACACCGCCGAA  
AGCAGGGGGTGCTTTGGGGCTGTATAAGATAAAGAGCCCCCTCATCTGTTTGT  
CGCTTGACCGACAGTTGATGACGCCCTTGGCAATGTCTTAAACAGCACTTTGAAACAGT  
GCGTTGGGCGAATTTCTGGATAAATGCACCAATTTGCCCGGGCTAATATCTTGATAAA  
ACATCGCCATAAAATAGAAAAATTAAGTTTAGGATTTTTTT

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SEO, ID NO:45

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the lbpB gene from *Moraxella catarrhalis***

CAGCTTGTACCATTTGGTGAATATATACCAATTTGGTGGTTTGTGGATATTTTACCAGGG  
 CTTGAGGGTGTGCGTAGCCTAAGCCGTGGCGATGATGAAGCAACCACCTCTCAATTTGGG  
 GCGGCGTGGGCGATACGATTGGTGGCGCAATTTGTTATGAGGTGGCATTCCTGAGACG  
 ACGCGTAAAAATGCACCTTGGCAGTAATTTTTTATTAAACCGTCTCAAACGATGCTTGGTTT  
 GGTACAACAGCAGGTCCTTTTGCACCAATTTACAAGATGCTGCAATTCGGAAGCTTGGAGCA  
 GGGCGATGTTTGTTCGCTGCAGAAAAACCAACGAGGTGACTGCTTAATTTGACATCAAGGA  
 CGGATTATCAAGCAGATACCGCAGTTTCAGCGAGATATTTGCGAGGTGATGTACCCAGT  
 TATGTTTGGACACACGCCCTTATATGTTTGGGGGCCATTCCCATGTGGGGGTTTCTTTTG  
 TGCTGTAATTTTCTTAGTATCATGGCAAGAAATGAAAAATACCACGCCCAACGAGAA  
 AAATTTATATACCGCTGATGTTGTGTGTAGACCGCTGAATTTGTGCGCAATTTGGGCGCTTAGAG  
 CATGAGCAAGATTAGCGTTGGTGAGCTTTGGTTGTTATTACTCATCAGCCTACCCGAAA  
 CTTGCCAAACATACCGGCCCAAAACCTAAACATACAATGGCTAAAAATTCAGAAAAATAA  
 CTTGCTGTAATTTGTAATCTTATGTATTCATGTGATAATAATTATCATTTAGTACCAAGAT  
 ATCCATTACTAACTTCATCCCCACTCTTAACAGTTACCAAGCGGTGAGCGGATTATCCG  
 ATTGACAGCAAGCTTAGCATGATGGCATCGGCTGATTGCTTTTTGCGCTTGTGTGTGTT  
 TGTGGGAGTGTAGTTGACTTACCTTATGTTGGTGATGCTTGGGCTGATTTAATTAATTTG  
 ATCAAGCGGTCTTCAACAACCAACCAACGAGATATCAC

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SEO. ID NO:46

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the *tbpB* gene from *Moraxella catarrhalis***

AGTTTGCCCTGATTTTGAGAGGCCACTGCCATCATGAATTTGTTGGCGTAACACCCACTCG  
TATTTCTTCTTCCGGTTTCCCTTTCCCTATGCCAACAGGGGATCACCGCGCCCGCATGGCA  
GCGCGCGCGTGGTCTTGGGTGCTAAAAAATTATGCATGATGCCACGGCAATTTCTGCACCC  
AAGGCAACCAAAAGTCTCAATCAGCAGCCGCTGTTTGAATTGGTCAATGTGATACAGCCTTAGG  
ATTTTAGCACCTTTAAGTGTGTGCTGGTCTTGATAGCGTTTCTTCAAGCCCATCAGGGCT  
GGCATCTCAGCTTCTGCCAAGGCAATCTCACGGCGACATAATCGGCTTAAACGGGATATCA  
CGACTTTTAACTCGGTGAAGTTTGGGTGGTACTTGGATTGATTGAGGTAGCGCATATCT  
TATCTCTAAGCTATTTTAAAGTATTTTAAACATAAATTTTGTAAGATTTGAGATAATTG  
ATGCTAAAAGTGTGAATGCCAACCAACCTCGCTAACACTAAGAAAGAACATTTTAAAGCAT  
AAAAAGCAAAATGGTGTCTTGATGGCTATTATAACAGTTTATTATGATAAAATTTGGGTAGAA  
AGTTAAATGGTGTCTGGGTGAAGTTTGTGGCTATCTCTTAATTAATTAATTTTAAAT  
AATGCTTTTACTTTATTTTAAAAATAGAGTAAAAATGGTGGCTTTGGGTTTTTATCTC  
ACTATGGTAGATAAAAATTGATACAAAATGGTTTGTATTATCACTTGTATTTTGTATTATAA  
TTTTACTTTTATTTTACAACATATACATAAAATCAAAAATTAATCACTTTGGTTGGGTGG  
TTTTAGACGCAAAATGGTTATTTTGGTAAACAATTAAGTCTTAAAAACGATACACGCTC  
ATAAACAGATGGTTTTTGGCATCTGCAATTTTGATCGCTCGCTTGTGATTGGTTGGGGTGT  
ATCGGTGTATCAAAAGTGCAAAAGGCCAACAGGTGGTCAATTG

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SEO. ID NO:47

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the *tbpA* gene from *Moraxella catarrhalis***

5 TTGGGGGCGGATAAAAAAGTGGTCTTTGCCCAAAGGGGCATATGTGGGAGCGAACACCCAA  
ATCTATGGCAACATCATCAAAATCACAAAAATACAACGACCATTTGGGGCAGACTGGGG  
GCAAATTTGGGCTTTTGGCTGATGCCAAAAAGACCTTAGCATTGAGACCTATGGTGAAAAA  
AGATTTTATGGGCATGAGCGTTATACCGACACCATCGGCATACGCATGTCGGTTGATTAT  
AGAATCAACCCAAAATTTCAAAGCCTAAACGCCATAGACATATCAGCCCTAACCAACCAT  
CGGACGCCAGGGCTGACAGTAATAACACTTTATACAGCACATCATTGATTTATTACCCA  
10 AATGCCACACGCTATTATCTTTGGGGGCAGACTTTATGATGAAAAAGTGCCACAAGAC  
CCATCTGACAGCTATGAGCGTCGTGGCATAAGCACAGCGTGGGGGCAAGAATGGGCGGGT  
GGTCTTTTCAAGCCGTGCCCAAATCAGCATCAACAACGCCATTACCAAGGGGCAACCTA  
ACCAAGTGGCGGACAAATTCGCCATGATAACAGATGCAAGCGTCTTTATCGCTTTGGCAC  
AGAGACATTCACAAATGGGGCATCACGCCACGGCTGACCATCAGTACAAACATCAATAAA  
15 AGCAATGACATCAAGGCAAAATTTATCAAAAAATCAAATGTTTGTGAGTTAGTCGCATT  
TTTTGATGGGATAAGCAGCCCTACTTTTGTGTTTGTAAAAAATGTGCCATCATAGACA  
ATATCAAGAAAAATCAAGAAAAAAGATTACAAATTTAATGATAATTGTTATTGTTTAT  
GTTATTATTTATCAATGATAAATTTGCCGTATTTGTCCATCACAACGCCATTATCATCA  
ATGCCACAGACAAATACGCCAAATGCACATTGTCAACATGCCAAAATAGGCATTAAACAGAC  
TTTTTTAGATAATACCATCAACCCATCAGAGGATTATTTT

SEQ. ID NO:48

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the *ompE* gene from *Moraxella catarrhalis***

25 AAAGACATTACACATCATCTTCAAACGCCCAACCATGTACCTCTGCCCCGTGGTCGCAC  
GCCAACGCTTTTTGATGCGGTGCGTTGGGTTTCAAGTGGCTTGCAATCATTGTTGTTTAT  
TAAAATTCATACCTTTGGTAGTTTGGCTTTACCTGATATGTCATTTGATTATCGAAACAA  
TAGCGAGTTGACCAAAACATCAATTTTAGCCATTGCCAAGCACTCAATATTACCGCTCA  
TAGCACCATGCTTGGTATTAATCATCACATAAAGATACTTTACATCCATTGGAATTGAC  
ATTACCCAAATCAGGCCATGCTCCTAAATTTATGATGATGAATTTGGTGCAAAACAAATCCATT  
30 GGCTTATTTTATCATCACTGTCTGCCGTCTGCCGATATTTTATACCAACCGTTTGTAT  
TGTTGGCGGTGAAAGCTCAGGGAAACTACCTTGGTGCAAAACTTGCCAATTATTATGG  
TGCCAGCATCGCACCTGAAATGGGTGCGATTATACACACACTCCCATCTCGGGCGGTAGCGA  
ACTTGCCCTTCAATACAGCGACTACGCATCCATTGCCATCAATCAGGCCAACGCTATCGA  
AACCGCTCGTACCACTGCCAGCTCTGCTGTACACTGATTGATCTGATTTTGGGACAAAC  
35 GCAAGCATTTTGTGAAATTTATGAAGGGCGAACGCATCCGCTTGTGCGAGAATTTGCTAA  
ACAAATGCGATTGGATTTTACGATTATTAGATAAATGTTGCTTGGGTGCTGATGG  
CATGCGTAGGGCTTGGTGATGATCATCAACGCAGTTTGTTCGCCAATAAATTGCTTGAGAT  
TTTGGCACGATATGATATTAGTTATCATATCATTATGACACCGACTACCACAAACGCTA  
40 TCTACAAGCATTAAAGCTTGATAGACAATCATATTTTAAATCATTTTACAAAAATTCATGA  
CAATTAATTAGGAAAAATCTGATGAAAATTGATATTTTAG

SEQ. ID NO:49

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the *uspa1* gene from *Moraxella catarrhalis***

45 GGATGTGGCATATCTGCCATCGACCCAATACACATCGGTGCGAGGCTATCAAGATGTGGT  
ACGAATTAATAGCCAGTCAGGTAAGGGCGGTGCTGCGTATATCTTGACGCGGCATTGTTGG  
TTTTAATTTACCACGCTGGACACAGATTGATTTTGTCTGCTGTTGTTACAGGCTTATGCGA  
AAGTATGGCGCGTGAACATAAACTGATGAGCTGCTTGAATTTTACCCAAGCGTATCT  
50 TAAGCAAGATAAATTCGCCCTAAGTGACTATACCATCAGCAATAAAGGCGATGCTGTCAG  
CTTCCAAGGCCAAGTAGCGACACCCAAAGCGGTGTTTGAGGTGATTGGTCAAGGCAATGG  
TGCGTTATCTGCGTTTATTGATGGCTTGGTGAAATCCACAGGCAGACAGATTGATGTCAC  
CAATTACGCCCGAACACGCGATCGATAACAAAACCCATCAAAAAACCGATACGGATAACCA  
AACCAGATGCCCGCGTGCCTTATATCCAGCTGTGCGTAGAGGGGCGAGTTTATTCAGGC  
55 ATCGCCACTTGCCATAGCACCGTATCCGCCATGCTAAAAGGTGCATTATCCGCTTTGGCA  
CAGGCGTGGTAATCTGACCCAATCAAAATCCTGCATGATGGCAGGATTTTATTATTAGT  
GGGCTGCCCAACAATGATGATCATCAGCATGTGAGCAATGACTGGCGTAAATGACTGAT  
GAGTGTCTATTTAAGAAAGATATCAATATATAAAGTTGACTATAGCGATGCAATACAG  
TAAAATTTGTACGGTTAAACATAACGACGGTCCAAAGATGGCGGATATCGCCATTACCA  
60 ACCTGATAATCAGTTTATAGCCATTAGCGATGGCATCAAGTTGTGTTGTTGATTGTCA  
TATAAACGGTAAATTTGGTTTGGTGGATGCCCATCTGATTTACCGTCCCCCTAATAAGT  
GAGGGGGGGGAGACCCAGTCATTATTAGGAGACTAAG

SEQ. ID NO:50

**Nucleotide sequence of DNA region (1000 bp ) up-stream from the *uspa2* gene from *Moraxella catarrhalis***

65 CCCCCAGCTTTCCGTTTGTGTGCTGCTGGTGTGCGGGCGGTACATACCATGCTGGTGGCTG  
CCGATGGTGTGGGCGTGTATCAGATATTGGGCGAGTCTATCGATGATGCGGTTGGGTGAAT  
GCTTTGATAAAACGGGCAAAAAATGCTCAAACTGCCCTATCCTGGTGGGCAAAATACGAAA  
AATTAGCCAAAAACGGCAACCCACACGCCCTATGAGCTGCCAAGACCCATGCAGCATAAAG  
70 GGCTGGATTTTTCGTTTCAAGTGGCATGAAACCGCCATTCAATCTCATCAAGACACAC  
CAAAACGCCCAAGCCCGCCACACGAGCAGACATGCCCGCAAGCTTTGAGTATGCGG  
TGTTGGATACTTTGGTCAAAAAATGCACCAAGCACTACAGATGACAGGCATTGCCGAC

TGGTGGTCGACGGGGCGTCTCTGCCAATCAGATGCTACGCCGCACCGTGACCGAGACGC  
 TCCGCCAAATCGATGCGTGGGTGACTATGCCCGACCGAGCTATGCACGGATAATGGTG  
 CGATGATCGCCTATGCTGGCTTTTGTGGGCTCAGCTGTGGACAGTCGGATGACTTGGCGG  
 5 TCCGCTGATTTCCCGATGGGATATGACGACGCTTGGCGTATCGGGTCATAGATAGCCAC  
 ATCAATCATACCAACCAATCGTACAAACGGTTGATACATGCCAAAAATACCATATTGAA  
 AGTAGGGTTTGGGTATTATTTATGTAACCTTATATCTAATTTGGTGTGATCTTTGATAA  
 AGCCTTGCTATACGTGAACCTAAATGGATATGATAGAGATTTTCCATTTATGCCAGCAA  
 AAGAGATAGATAGATAGATAGATAGATACTCTGTCTTTTATCTGTCCGCTGATGCTT  
 10 TCTGCCTGCCACCGATGATATCATTTATCTGCTTTTAGGCATCAGTTATTTACCGTGA  
 TGACTGATGTGATGACTTAACCACCAAAAGAGAGTGCTAA

## SEQ. ID NO:51

Nucleotide sequence of DNA region (1000 bp ) up-stream from the omp21 gene from *Moraxella catarrhalis*

15 GAGTGAACCTTTATTGTAAATATGATTCAATTAAGTATCAAAATCATCAACGCAGCATC  
 AGGGTTTGGTAAATCAATTTTTTACCATAATTATAGCCATAACGCACAGCAAGCGTAGT  
 TATGCCAGCGGCTTGCCCTGATAAAATATCATTTTGGAAATCACCACCAATATGGCATC  
 AGTCGGTGCGATGCCAGTGATTGACACAGGTATAATAAGGCGTTGGGTGGGGCTTTT  
 20 GACGCTGAGCGTATCACCGCCAATCAGTTGGTCAACAGTGTGAGCCATCCAAATGTGA  
 TAAATTTTAGGCAAAATACGCTCAGGCTTATTGGTACAAATTGCCAAATAAACCCCGC  
 TGCTTTTAAATCGTTCAAGCCCTTGTATAACCCCTGCATAGCTTTGGCGTATTTCAATTGT  
 TTTATGGGCATATTTCTGCCAAAAATACTCATGGGCATGGTGAATCATAGTCGTATCATA  
 GATATGATGTGCTTGCATTGCTCGCTCAACCAATTTAGCGAACCATTTGCCACCCAGCT  
 25 TTTGATGATATCAATTGGCATAGCGGTAAGTTAAGCTTGGCATACATGCCATTGACCGC  
 CGCCGCCAAATCAGGGGCACTATCGATAAGCGTACCATCCAAATCAAATATAATCAGTTT  
 TTTGCCAGTCAGCATGTTTGCATGCTTTTCCCTTATTCTTAAATTTGGCGGCTGTT  
 TGGTATTTTTTAAATCAGTCAATTTTACCATTGTGCATATAATGACAAAGTACAAATT  
 AGCAATATTTAGTGCATTTTGGCGAAGTTTATGAAACTGGTCATTGGTTGCAAAA  
 30 CTTTACACAGTACCTATAAACTTGCACAGTTAATAAGAAATATTGTGTTACTATAGGGG  
 CGTCATTTGGAACAGACAGTTATTTGTAAATAGTTATTTGCAAAAGACGGCTAAAAGAC  
 AGAACAGCGTTTGTTCAGTGATTAAC TAGGAGAAAAACA

## SEQ. ID NO:52

Nucleotide sequence of DNA region (1000 bp ) up-stream from the omp106 gene from *Moraxella catarrhalis*

35 TTGATCGGTTTTGCCCCACTGTTTCATGATTTACTCAAAACAGGCGGCTTGATCGTGCTG  
 GCAGGTCTGACCCAAAACCAACCCAGCGGTCATCGATGCCCTACTCGCCTTATGTTACG  
 CTTGATACGCCATTTTGTATGAGATGCCCAAGACTGCCATTGGCAACGCCCTAAGCGGC  
 40 ATCAAACTTACCAACCCATAAGCGATATGCCATGAGCCACAAACCTAAGCCAAACCGCT  
 ATATCAACAAGTTGAGCAGACCCCAAGCGTTATTTTGGACATTGGCGGATGCTCATAC  
 TCATGATGTCTATGCCACTTTTTTGGCCGAATTTGAAAAACCGCTGCTCATCGCCGCACT  
 CAATCACACGACCGCAATCAGTCAAAAACCGCCCAATCCTTGGTATCAATCGTGCCAC  
 ATTACGCACCAAAATGAAACCCATCACTTACTTTAGACCGCCAGTTATCGCCATGGATA  
 45 TGGCGAGGTGTGCTCGCCTGCCGTATGATGGCGATGACACCCCATTTGCCCATATCTGC  
 ACGATTTGACATGATTTAACATGTGATATGATTTAACATGTGACATGATTAAACATTGTT  
 TAATACTGTTGCCATCATTACCATAATTTAGTAACGCATTGTGAAAAATCATTGCCCCCT  
 TTTTTATGTGTATCATATGAATAGAAATATTATGATTGTATCTGATTATTGTATCAGAAT  
 GGTGATGCCCTACGAGTTGATTTGGGTTAATCACTCTATTATTGATATGTTTTGAAACTA  
 50 ATCTATTGACTTAAATCACCATATGGTTATAATTTAGCATATGGTAGGCTTTTGTAAA  
 AATCACATCGCAATATTGTTCTACTGTTACCACCATGCTTGAATGACGATCCAAATCACC  
 AGATTCATTCAAGTGATGTTTGTATACGCACCATTTACCCTAATTATTTCATCAAT  
 GCCTATGTCAGCATGTATCATTTTTTTAAGGTAAACACC

## SEQ. ID NO:53

Nucleotide sequence of DNA region (1000 bp ) up-stream from the HtrB gene from *Moraxella catarrhalis*

55 ACTATTCTGCTTTTTGTTTTTCACGAATGCGAATGCCAACTCAGCCAACTGGCGATTAT  
 CAACTTCAGCAGGTGCTTCGGTCAATGGGCAATCTGCCGTCTTGGTTTTTGGGAAGGCGA  
 TCACATCACGGATTGAGCTGGCACCACCATCAGCATATCAGGCGATCTAGACCAATG  
 60 CCAAACCCGCTGCGGCGGTGCACCAAAACGCAATGCATCCATCAAAAACCTTAACTTAA  
 GCTCTGCTTCTTCTTAGAAATACCAAGGCATCAATACCGCCTCTTGCATGTCAACCG  
 TATTAATACGCAGCGAACCGCCACCAATTTCTGTGCCATTAGTACCATGTCTAGGCAA  
 TGGATAGGGCGGTTTCGGGACTTTGTTTGGATTCTCAACCGAGCCTTTGGGCGGTGTA  
 AAGGATGATGAACATGATGCCACTTACCATCATCAGTTTCTCAACATTTGGAAAATCAA  
 65 CGACCCAAAGCGGTGCCCATTCACAGTAAATAAATTTAAATCAGTACCGATTTTAAAC  
 GCAATGCAACCATATGATCATTTGACGATTTTGGCTTTATCGGCACCAAGAAAATGATAT  
 CGCCAGTTTGGGCATCGGTACGCTCAATCAGCTCAATCAAAACCTCATCGGTATATTT  
 TAATGATGGGTGATTGTATCTGATTCTTTTCAACGCCATTATGATATTGCTTGGCT  
 70 CATTGACCTTAATATATGCCAATCCACGAGCGCCATAAATACCAACAAATTTGGTGACT  
 CATCAATCTGCTTGGGACTCATGTACCGCCATTTGGAATGCGTAAGGCAACACACGGC  
 CTTTAGGATCTTTGGGCGGGCCCTGAAAATACTTTAAATTAACATGTTGCATGATGTCAG  
 CAACATCAATAAGTTTTAAGGGAATGCGTAATCAGGCTTATCTGAGGCATAATCAGCA

TGGCATCTGCGTAAGTCATGCGGGGAAGGTATCAAACCTCA

SEQ. ID NO:54

5 Nucleotide sequence of DNA region (1000 bp ) up-stream from the MsbB gene  
from *Moraxella catarrhalis*

10 TGGATCATATCTTTATTAATGGTACTGTTTAAACCTGTATTTTAAAGTTTATTGGGTCA  
TATTTTCAAGCTCATCCCATCGCTCAAGCTTCATCATCAAAGCTCATCAATCTCTACCA  
ATCGCTCACCAGCCTTCGTTGCTGCCGCCAAATCGGTATTAACCATGAACCATCTTCAA  
15 TCTTTTGGCAAGCTGTGCCTGCTCTTGTTCAAGTGCAGCAATTCATTAGGCAAACTCT  
CAAGTTCACGCTGCTCTTTATAGCTGAGTTTGCCTTTTGGGCAACGCTGATTGAGGTG  
GTTTGATTTGGATGGGTTTCAAGCGGTTTGTGCGCTTAGGTTTATTGCTGTGGCGTGAT  
GAGCAAGCCATCTTTTATGCTGTTGTACATAGTCTTCATAACCGCCAACATATCCAAAA  
CGATACCGTCCGCTACTTTATCAGTATCAAATACCAAGTTTGGGTAACAACATTATCCA  
20 TAAAAAGCAGGTCATGGCTGATGAGTAATACCGTGCTTTAAATTTGACCAAAAACTT  
CTAAAAAGCTCAAGTGTGCCATATCCAAATCATTGGTAGGCTCATCAAGCACCACAAATCT  
TGGCAGGTTTTAGCAATAATTGGCCAATAAAACGCGTGCTTTTACCGCTGTATAGTG  
CTTTAACAGGTGTGCGAGCAGGATTGGCGTGAATAAAAAATCTTGCAATAGCTTAAAA  
TGTGCGTAGTTTTTCCACCAACATCGACATGGTCAGAGCCTTCTGAAACATTATCTGCGA  
25 TAGATTTTTCAGGGTCTAGGTCGCTCTTGAGTTGGTCAAAAAAGCAATATTAGATTGG  
TGCCAAGCTTAACTGAACCTGACTGAATCGCTGAATCATCAAACCAAAATGCTTTTAA  
TTAAGGTTGTTTTACCAACGCCATTTTGCCAATGATACCAACTTTATCACCACGAACAA  
GCAGCGTTGAAAAATCCTTAACTAAGGTTTATTGTGCTAT

25 SEQ. ID NO:55

Nucleotide sequence of DNA region (1000 bp ) up-stream from the PilQ gene  
from *Moraxella catarrhalis*

30 CAACTTGAAAATCAGCTCAATGCTCTGCCACGCACAGCACCAGTGAAGCGAGATTATCGGA  
ATGATAAATACCAAGCACAAGCGGTTAATGTGCAGGTGGTGAGTGCATCAGTTCAAGCA  
GGTCGTGAACAGGATTATTATACCGAACGCCCTATCGCAGTGAGTGCGACAGGGGATTAT  
CATGCTTTGGGTGCGATGGTTACTTGAGTTGTGAGAGGCTAACCATTTGCTGACAGTGCAT  
GATTTTGATCTGAAGGCTGGTTGAACCATCAGCTGATGATGTTGTTGAGATGAAAACT  
TATCAAGCGAACAACGCCCCAAAACAGTTGCTCAGCAGGTGCCTGATGTTCAATGAATA  
35 TTATCGGTGGGGCATTTTGGGTGCTTGGATTGGGTTGGGATTGGATGTGCTGATAGCAC  
CAGTCAAGTTTGTGATGATAAGCTTGACATATTACCCATGAAGAGCGTATGGCGATCAG  
TGAGCCTGTGCGGATACCTTATCTGTGCCGATGATATATCAGCAAGGCAAGATCCTTT  
TATCAATCCTTATAGAAATGTTGAGGTTCTTGATACCAATCATGCCGCTGATCAGCAAGA  
TGAGCCAAAAACCGAATCTACCAAAAGCTTGCCCTATGGCAGACACTATGCCATCTCAGCC  
40 ATCTGATACTCATCAGTCTGCCAAGGCTCAGGCACAAGTCTTCAAAGCGATCCGATAGT  
CATTGATACCAACCGTGTTCGAGAGCCTTTAGAAAGCTATGAGTTATCAAGCCTACGCTA  
TCATGGTCGTATTTTGTAGTATGTTAGACTTGTGGCACTCATTATGAGTCCTGATGGCAT  
CGTTTCATCGTGTGAGTACTGGACAATATCTTGGTAAAAATCAGGAAAAATTACCCATAT  
TGACAGTCGTACGATACATCTGATTGAAGCGGTGCTGATACACAAGGTGGCTATTATCG  
45 CCGTGATGTAAACATTCAATTTATTTCATAAGCAATGACAC

45 SEQ. ID NO:56

Nucleotide sequence of DNA region (1000 bp) up-stream from the lipo18 gene  
from *Moraxella catarrhalis*

50 TTCATGCAACAGCGACCATCTTGGCCGATGATACCATCCTGCTCACCTAAGAAAAATCAG  
TTTATCAGCTTTCGAGGGCAATGGCTGTGGTCAGTGCTACATCTTCTGCCAATAGATTAAA  
AATTCGCCCCGTAAACGAAAAACCTGTCGGTCTTAGTAGGACAATATGGTCATTATCCAA  
ATTATGGCGAATGGCATCGACATCAATTGAGCGTACCTCACCTGTCTGATAATCCAT  
ACCATCTCTGATGCCGTAAGGGCGAGCGGTGACAAAAATTACCGAAATGGCATCAATACG  
55 AGATCCGTACATTGGGGAGTTAGCAAGCCCATCGACAGCCGAGCTTCGATTGTAGACG  
AATTGAGCCGACTGCCCTCAAGATGGCAGGCATAGATTATACGGTGTACACGCACATT  
CTCATGTAGGTTTATATCAGCTTGCGATTTTGTAAATTTTTTCCACTTGTGGCGGTAC  
ACCATGCACAAGCACCATTGATGCCAAGCTGTGTAGCAGTGCAAAATCATGAATCAG  
CGTACTAAAATTGTACAGAGCGACCGCTCATCACCACATAACCAAAAGGTTTGGC  
60 ACGATGGGTGTTAATGTACGGGGCAGAATTACGAAACCAATGCACAGGTGTGAGTGCAGG  
AGTGTCTGATAGGTGCTGACAGAATTCATGAATGCTCCAAAGAGTCAATGGCTGGTAAA  
ATAAGAAATGGCGAAGATATATGGCGAGAGCGTCTGATGTTGGTCAAATGTCCCATTAAT  
AACTATCAAGATACCATCATACCATAGCAAAAGTTTGGGCGAGATGCCAAGCGAATTTATC  
AGCTTGATAAGGTTGGCATATGATAAAATCTACCATCATCGTCGCCAGTTTTGGAGCATGT  
65 GTAAGTAGTTACCATTAATAACAGTCAAGAAATTCACACCGTCAATCAGCTGTGCTATG  
CTTATGGGCACATAAACTTGACCAACACAGGATAAATTTA

SEQ. ID NO:57

Nucleotide sequence of DNA region (1000 bp ) up-stream from the lipo11 gene  
from *Moraxella catarrhalis*

70 GGCATACTTTGGCCATGCTTTATTTTGGCATAACTGCTATAAGCCCATTTGCTACTTTTAA  
TCATTTATCCATATGTCCAAATAATGTGCTTTATGTAATTTAGGCACACTATTAACCTCGTG  
CCACTGTTAACATTACGATAAAAATCTTAACAATGAATCAAAGCATCGTATTGGCTGTT  
AAATGATAAGCTTATATTTATTTAAATTCAGACTAAATGATTGTAATATGGACATATCAA



5 GGTGAAATCAAAAATTTTGGAGAGTTATGTACGATAATGATAAAAAATTGACCACCATC  
 TTAGGGGTGGTTGTATACGGTGTCTTATATTGCCATATGGTTGGTCAGTGGCTATATTTTA  
 TGGGGCTGGATTGGTGTGACAGGATTACTCGTGCAGTACTTTGGCTGATCGCTTGGATG  
 ATTGTGGGTACGATTGCTGATAGAATTCTGATACCGATTATTTTGACCGTCTGGTTGGG  
 10 TATTTTCTATCTTTTGGAAAAAGGCGATAATTTGGTTATTTTTCACAAAAAATCAT  
 GATTTTTTTTGTAACTATCTAAAAATCAATTATGTTATATTATGTGATAAAAGATGGG  
 CATGCTTAAGTTTGGATTGCAAAAATCCTAATATCATCACTGACCAAAGCTGTGATGAT  
 ATCAAACTTTATCAAAGTTCTTAGGGTATTATCAAGATATCATACCAAATGAATACTTA  
 CCCAACTTACTATAAAAAATCAATGATATGACTGTGATTTTATTATCATAGATACAAAAA  
 TCAAAACGCATGAGCCAAAGGTATGATGAATGAATACAAAATTTGCGACACATTATGACA  
 ATCTAAATGTGCGCCAGAAACGCTGACATTGCGGTGATTGGTGGGATAGGGGTCAAGCCA  
 GTGCGATTAAAGCTAAATTTTTATGTGGCAATCGCTGACTTTATTTTATTGTGCCAGTT  
 GGAACAATTCGTGGTCTAATGTATTATTTAAGGAGATAA

15 SEQ. ID NO:58

Nucleotide sequence of DNA region (1000 bp ) up-stream from the lipol0 gene  
 from *Moraxella catarrhalis*

20 TCTGGTCTACATCCCAAATTTTACACAAGAAACACTAAAGACAGTGGAGCAGATGACG  
 CTCAAAAAGGCATCTTATAGTAATTTGACAGTTAATTTTCGTCAAGTCTTGTACAAAAA  
 TACACCATCGTCAAGAAGTTTGTACCAATTAAGCACAATCATTTTGGCAGCAGCTGTC  
 AAGCAATGCTTCAGGCAAAATTAGCTGCTGGTAAAGATACTTGGGTCAATGCAATCGCA  
 TCAACCTTCTTGTGTCGGTTGAAGCGATAAGTTTGGCATCTTGCCAAAATTGACCATGGT  
 25 TTAGACCTTTGGCGTGGCTTGTGGTATCGCTCCACATGTCGTAGAGTAGATATTCGGTCA  
 TATCAAAAGGGCGATGGAAATGTATGGAATGGTCAATACTAGCCATTTGTAGACCTTGTG  
 TCAATCAGGCTTAGCCATGACTCATTAAACCTGTGCTGACCAATAATAATCAGACACAA  
 ACGCAAGTAGTGCTTGAATGGCAACTGGCTGCTCCCAATATCAGCGATACGCACCCC  
 AATTGGCTTGGCGTGGACGCTCAGGCTTGGGTGTACAGGGTCTCGTGGTGTGACGGGGC  
 GGATTTGACATGACGCTGACGCATAAATCTTGTCTTGTAGTGGTTCGGGAATTTATGTA  
 30 AATAATCCGCTTTGAGTTCTTGTCTGGTTTTTAGGCTTTTCAAGGGGTGGATAATCAGGCA  
 TGGTTTCTTGGTAAATCAAGCCCGCTTCCATGGGTGAAAATGAGGCAATCATCGAAAAA  
 TGACCTGTTTATGGTGTATGATTACCGTTTTTGTGCGGTGGTGGCAGATATTGCACCG  
 CAATGACTTCTCGAGCTGATAAACTGCGTCCATCACGTAAGCGCGTACTTGATAGATGA  
 CTGGTAGACGAATATCGCCACCTCGTAAAAATAACCATGTAGGCTATGACAAGGTTTAT  
 35 CAATCGTTAATGTGTTAGCACCAGCAAGCAGCGCTTGGGCA

SEQ. ID NO:59

Nucleotide sequence of DNA region (1000 bp ) up-stream from the lipol2 gene  
 from *Moraxella catarrhalis*

40 TAAAATGACCTTACAAAATAAAATTATATGTTCAAAAATCGCTTAAGTATTGAAAAAGC  
 TATAAAAATCTTATTAAGCATAAAAGATATTAAGCATAAAAGACGAGAAAAAGAGC  
 AAGCGTCAATGTAGATATTTATATAAAAATTTATGAAATTTTCAATTTTTATCGATT  
 GATTCAGCTTGGCTATCGGTGGTCAACTTTGGCTGCCAAGACATCGCCGGCTTTTTGAAA  
 AATCATCACAAATGGCAACATGATGATGGTTGAAATCCACTTGACATATACCATGTTGCG  
 45 ATGCTCACCATAGTTAATCGCAAGGCTTCCCAAGCCACCACGCCAACACACCTGCCAT  
 TGCAGAATAACCAATCAAAGACACCAAGGTCAATGTGACCGCATTAATCAAAATGGGCAG  
 GCTTTCAGCAAAATAGTATTGCTGACAACCTGCCAATGCGTGTGACCCATAGATTGGC  
 AGCTTCGGTCAGTCTGTGGTACTTCTAATAAAGCATTGGCACTCAAGCGTGCAAAAAA  
 TGGAATTGCTGCCACACTCAAAGGGACGATGGCGGCTGTTGTGCCAAGGGTGTCCAC  
 CAAAAATCGTGTGACTGGCATGAGAATAATGAGCAAAATAATAAAGGAACGGAGCGACC  
 50 AATATTAAATAACATCCAAAATTACAATAACACTGCGATTTCAGGATACGCCCTTT  
 ATCGGTTAAAAATGCCAAAAACCTATCGGTAGCCCAACCAAAACAGCGATGGCAGTGGC  
 AGCAAGCCCCATATAGATGGTTTCCCAAGTGGATTGGGCAACCATCTCCACATTCTTGG  
 GTGCATTTCATGACAAATTTTGTGACGATTTCATTCCACATAGCCGATAATCTCAATAT  
 55 TGACCCGATGGGTGGTTAAAAATTTATGCTTGCATGACCGAGGTGCCTTACCAGATAA  
 GCTCAGCAATGGTAAAGCCAAATTTATATCACCTGCATAA

SEQ. ID NO:60

Nucleotide sequence of DNA region (1000 bp ) up-stream from the lipol7 gene  
 from *Moraxella catarrhalis*

60 AGTAACAATGGTAACAAATACAGCAGTGTGCGACAGTCTCAGTACGATGATTCTGAAT  
 TTGAATATGCAGGATTTGGATACGATTTGTGGCATGTCTTGTGCGATAATTTAATTGTTA  
 TGATTATATATGACCGTATTGGTTTTATAATTATCAGCAAAATGATGGCCATGCCGTGCTG  
 ACCAAATACCGTTTTATAGTGTGGGGATGCCATCCTTTATAGTGTGGGGATGCTATCC  
 TAACTTAGTGATGGCGGGCGGGTGTGGTTTGGGTAAAAAAGGTGCAACACCAG  
 65 GTAAAATGCTCTTTGGGCTGCAAGTCCGTGATGCCAAAACAGGGCAATTTATCAGTGTGC  
 CAAGGGCATATTGCGATATTTAGTTATCTGATTTCATCCGTGATTCTTTGTTTGGGAC  
 TTATTTGGGTGGTTTTGATAAGAAAAACAAGGCTGGCATGATAAAATTGCCAAAATCTG  
 TTGTGGTAAAAACGCTTCGCTGATGGGTGCGCCAGTTAAACAATAAAACCATCAAAACGCA  
 GCAGGGCGATGTGTTTGTGAGCAGTTGCGCGTAGATAAGCTAAACAAGCAGGCTATGAAAT  
 70 TATTTTAAACCACTTTTACCACCCCATTTGTTGGTGAGATTGATATTATCGCCAGACAGCC  
 TTTGGAGCAATCGCACCCTTTGGTGCAGCCAGATTTTGTACGGTATTTGTTGAAGTGGC  
 TAGCCGAACAAGTTCTGTGATGGTACAGCGCTTGAGAGTGTTACCTCAAAAAAGCAGGC  
 AAAAATCTACCGAACAGCAGAACGATTTTAAATCAATTATCCCAATATATTGATGATGC  
 75 ATACCGTTTTGATGTCATGGTTTTGATTTGGTTGATGGATTGATTGAACATGAATGGAT  
 AAAAAATGCGTTTTGATTGGCTCAATGGTGTGAATTAATCAATCAAGCAATCCGTAG

CTTTACTATAAGATATATCCCAGTAATATGGAACATAGCA

SEQ. ID NO:61

Nucleotide sequence of DNA region (1000 bp ) up-stream from the lipof gene  
from *Moraxella catarrhalis*

5 C G T T T A G C T T C A T A C G C A G A C C T T G T G C A C C T T C G G G C A A C C G A A G C A T C A C G C C A G C A T  
C A C G C A T C C G C A C A A A A C C C A T C A T G C C A T C A A T T T C G C T G C T G A T A T G A T A T A C C C C C A  
C C A A A G T A A A C C G C T T A A A T C G T G G A A T A A C G C C T G C T G C T G A G G G T G A G G C T T C A G G C A  
10 A A A C C A A G G T A A C C T T A T C C C C C A A C T T A A G T C C C A T G T C A G A G A C A A T G G A C T C A C C T A  
A T A T A A T A C C A A A C T C G C C G A T A T G T A A A T C A T C C A A A T T G C C T G C G G T C A T A T G C T C A T  
C A A T G A T A G A A A C T T G C T T T T C G T A A T C A G G C T C A A T G C C A G A A A C C A G A T T C C A G T C A  
C C T G A C C T T C A G C G G T T A A C A T A C C T T G T A G T T G A A T A T A A G G G G C A A C T G C T T G C A C T T  
15 C T G G A T T T T G C A T T T T G A T T T T T C G G C A A G T T C T T G C C A A T T T G T C A A A A T T T C T G T T G  
A G G T A A C T G A A G C T T G A G G C A C C A T G C C A A G A A T G C G T G A T T A A T T T C A C G G T C A A A G C  
C A T T C A T G A C C G A C A A A C C G T G A T A A G C A C T G C A A C C C C A A G C G T A A G C C C A A T G G T T G  
A G A T A A A A G A A T A A A G G A A T A A A G C C A T T T T A C G C T T A G C T T T G G T A T A T C T A A G C C  
C A A T A A A T A A C G C C A A G G G A C G A A A C A T A A G C T G T G T T C C A A C G A C C C A A C C G T G C T A G  
20 T T T A G C A C T T T T T G G A C A A A T A C C A A C A T C A C A T A A C A A T G A A T C A T C A G G T T G G T T  
T T G T T G C G C T T G T G A T C T G T A T G A T A A G T T C T T G C T A A A A C A G C T T T T T A T G T C A G A  
A T A C A G A A A A G G T A T A T A C T T A T A T T T T A C T T T A A A T A G A T C T G C T T T T T A T A C C G A  
T G A T T T G C A T G A A G T T T A T C G G T C T G A T A T G C T G G A T A T A A G T T A T C G G C T T G A T A T A  
A A T T T A A T T A A T C A T C A A A T T T T A A G G A A T T A T C A T T A

SEQ. ID NO:62

25 Nucleotide sequence of DNA region (1000 bp ) up-stream from the P6 gene from  
*Moraxella catarrhalis*

30 T A A G G A T A C C A G A T T T T G G C T T G T C A A T C G T T G T T A A T C A T T G T A A C G G T T T A T A G T G  
A T T G T C A A T T A A T A A G G G T A A A A A G T A T T A T C A A G T A A T A A T C T T C T T A T A T G T G A A  
T A T A A T G A C A A A T T T A T C A C A T T T T A C A A G A T T T T T A T C A A G A T T A G G A T A T G T T C C  
A G C T T A A T T A T A G T G A T G A G C G T G T G A T T A T T T G G C A T C G T T A A A T T A T G A G T G C T A A  
A A T T G C C A A A T G A T T A A A T T T T G C T A A C A T G A T A G C C C C T T T G G T A G G C T T A T T T G G T  
A T T G A T G A G C A A T A A T A A T A T A C C G A G T T A A T G G A T T A A C T T A A C A T A C G C C A A A A C T  
35 T A A C A C G A A A A G T A G A T G A T T A T G A C A G A T A C A G T A C A A A A G A T A C A G C A C A G T C C C C  
C A A A A A G T T T A T C T A A A A G A C T A C A C G C C C C A G T A T A T G C A G T T A A T A A A G T G G A T T T  
G G A T A T C C G C T T G T T T G A T G A T C A T G C T G T C G T T G G T G C C A A C T T A A A T G A C A C G A G C  
A C A C G C A G G C G A C T T C G G C T T C T T G G G C G A G A T T T A A G C T T A A A A G C A T T C A C C T A A A  
T G G T C A G G A A T T A G A T G C G A G G C G T A T C A T C T T G A T A A G G A A G G C T T A A C A A T T T A G A  
40 T G C A C C A G A T G T C G C A G T G A T T G A G A C A T T G G T T G A G A T T T C A C C A A A C C A C A C A C  
A C T T G A A G G G C T A T A C A A G C A G A A C A G G T G A T G A T A A G A T G T T T G T G A C A C A A T G C G A  
A C C T G A G G G T T T C G C A A A A T C A C C T T T T C C C T G A C C G C C T G A T G T T T G A C A G A A T A  
C A C C A C G C C T A G A A G C C A A A G C A T T T A A A A C C T T G C T T G C C A A T G G T A A T T G G T  
T G A G T C A G G A G A T G T G G A T G A A A A T C G C C A T T A T A C C A T T T G C A T G A T C C T A C C A A A A  
A C C A G C T A T C T A T T C G C C G C T G T C A T T G C C A A T C T A G A A G

45 SEQ. ID NO:63

Nucleotide sequence of DNA region (1000 bp ) up-stream from the MsbB gene  
from *Haemophilus influenzae* (HiRd)

50 A A A T C A A G C G C C T G T G C C T G C T G G T G A T G G T T G T G G A G A C G A A T T A T A T T C T T G G T T T G A  
A C C G C C A A A A C C A G G C A C T T C A G T G A G C A A A C C T A A A G T T A C A C C G C C T G A G C G T T T T T  
G T G C C A A C A G A T T T G A A C T C A C C G A A T C G G A G A A T G G T T A G A A T A G C A T T G A G G T A A  
A T C A A T A T G G A T A T C G G C A T T G A T C T T T A G C A A T A T T G T T T G T T G G T T T T G T C G C A  
T C A T T A T C G A T G C A A T T G C T G G C G G T G G T G G A T A A T C A C C A T T C C A G C G T T A C T C A T G  
A C A G G T A T G C C A C C A G C A A T G G C G T T A G G C A C C A C A A A T T G C A A G C T A T G G G C G G T G C A  
55 T T A T C C G C A A G C C T T A T T T C T T G C G A A A A G A G C G G T C A A T T T A C G C G A T A T T T G G T T T  
A T T T T G A T T T G G G T T T C T T A G G T T C T G C C C T A G G T A C A T T A T A A T T C A A T C A A T T G A C  
G T G G C G A T T T T C A A A A A A T G C T T C C T T T T T G A T T T A G C C A T T G G T C T A T A T T T T T A  
T T A C T C C T A A A T T A G G T G A T G A A G A T C G A A A C A A C G A T T A A G T A T C T G T T A T T T G G T  
C T T T A G T T A G C C C A T T T T A G G T T T T A T G A T G G C T T C T T T G G G C A G G G A C T G G C T C A  
60 A T C A T G A G T T T A G C C T G T G T T A C T T T G C T A G G A T T A A T C T C C C G A A A G C G G C A G C A C A T  
G C A A A A G T G A T G A A C T T C A C T T C G A A C C T T G C T T T T G C A C T T T C T T A T T G G G C G G A  
C A A A T C T T T G G A A A G T G G G T T C G T G A T G A T G G C T G G G A G C A T T T A G G T G C A A A T T A  
G G T G C C A A A T G G T G A T G A C G A A A G G T A A A A C C T T G A T T C G A C C G A T G G T T G T A T C A T G  
T C T T T A T G A T G A C G G C T A A A A T G G T T A C G A T C A G G G T G G T T C A T T T T A A T T C G G A  
65 A A G C G C G C A A A G T G C G G T T A A A A T T A A T T A C A T T T A T T A

SEQ. ID NO:64

Nucleotide sequence of DNA region (1000 bp ) up-stream from the HtrB gene  
from *Haemophilus influenzae* (HiRd)

70 T T G A A G T C C C C A A T T A C C C A C C A C A A T T C C T G C G G C A A C A T T G G C T A G G T A A C A A G A T T  
C T T C G A A A G A A C G T C C A T C T G C T A A T G T G G T T G C T A A T A C A C T A A T G A C A G T G T C A C C G G  
C T C C G C T C A C A T C A A A C A C T T C T T T G C A A C G G T T G G C A A T G A T A A G G C T C T T G A T T T G  
G G C G T A A A T G T C A T G C C T T T T C A G A A C C G T C A C C A A A A G T G C G G T T A A T T C A A T A T  
C A G A A A T T A A T T T A A C C T T T C T T A A A T C T C T C T G T A T T A C A T T T A C C T A C A A

CGGCTTCAAATTCAGACATATTGGGTGTCAATAATGTAGCCCCACGATAACGTTCAAAT  
 CAGTTCCCTTTGGATCGATCAACACAGGCACATTCGCTTTGCGTGCATTTGAATCATT  
 TCTGAACATCTTTAAGCGTGCCCTTTGCCGTAATCAGAAAGAATCAAAGCACCGTAATTTT  
 TCACCGCACTTTCTAATCTCGCTAATAAATCCTTGCAATCTACATTATTGAAATCTTCTT  
 5 CAAAATCAAGCGGAGCAGCTGTTGATGACGAGATAAAATACGTAATTTAGTAATGGTTG  
 GATGGGTTTCTAATGCAACAAATTAACAATCAATCTTTTGTTTTCTAATAAGTGGGAAA  
 GTGCAGAACCTGTCTCATCTTGTCCAATCAATCCCATTAAGTGAACGGGTACATTGAGTG  
 AAGCAATATTCATCGCCACATTTGCAGCACCGCCCGCGCGTCTTCATTTTCTGTACGC  
 10 GAACTACTGGCACTGGTGCTTCTGGTGAAATACGGTTGGTGCACCGAACCAATAACGAT  
 CAAGCATCACATCGCTAATACAAGTACTTTTGCTTGCTTAAATCTGCTGAATATTGAG  
 CCATTTTAAATCTCTCTATTGTAATAACCAAATTTGTGGCGATTTTACCACAACCTCAA  
 TTTACGATAAATACGCCCTTAACCTACGTGGAAAGAACA

SEQ. ID NO:65

15 Nucleotide sequence of DNA region (1000 bp ) up-stream from the protein D  
 gene from *Haemophilus influenzae* (HiRd)

AGCAATAATTATAGCTGGAATATTCTTTAAAGATGAAAGAGATCGTATAAGACAAAAAGA  
 ATTTTATATTGGAGAATTATTAGCAATTATTGGTTCGCTAATATTCTGTAATAAATAGTTC  
 AAATATATGATGAAATACAGACTTTTTCTTGGGGCAATATTCTTTTACAGCTATTTT  
 20 TATTCAATCTGTACAGAATTTAATTGTAAAAAAGTAGCCAAAAAGATAAATGCTGTTGT  
 AATAAGTGCATCGACAGCAACAAATTTCAAGGATATTATTTTATGTTAGCTTTAATAC  
 TAAACAAATATATTATTACAAGATGTTGGCATTGGAATGTTGATAGGTTTAGTTGCGC  
 TGGCTTTTATGGGATGCTAACAGGGATGTTGATGGCTTTTATATTGTTCAAAAAACAGGG  
 AATCACTGTTTTTAACTTTTGAATTTTGAATTTTCACTTTTCACTGCGATAATAGGTTA  
 25 CTTAACATTAGATGAAAGAATAAATATCTATCAGGGAATTAGCGGTATTATTGTAATTAT  
 TGGTTGTGATTGGCATTAAAAAGAAAAACAAGGAGTGTGATATATAAAGTAGATGAT  
 GTTGGTGGAAATAGGTATAGTTAAATATCTGGTTCAATTGGTTTTATTAAGGGCGTTAGCA  
 ATTTCCATTTAAGTTTATGTTTGAATTAGATATTTGGGAAAAGATGGAAGAATAAAGC  
 TGTAAATATGCTGAACATATGAACTATACCAATCTCAAAATAAATAAATCTGCTG  
 30 GAAATGATTATAAATCTCTAATCTAATCTGATAGAGAGGATAATGACTATCAATCAGAAA  
 GAATGATTAAAGCCATTAAAAATATTATTCATTGTATGACTAATAATCATCAACCTATT  
 CAAGTGCTGAAACATCTTTAGAACTATTAAATATTACGGAATAAATAATTCTGTTA  
 AAATAGGTAATGATCTTAACAATATATAAGGAGAATAAGT

35 SEQ. ID NO:66

Nucleotide sequence of DNA region (1000 bp ) up-stream from the Hin47 gene  
 from *Haemophilus influenzae* (HiRd)

TAAATACTCCAAATAAATTCAGATAACGTGGTCTGTAAGACAAAAAATAAAAAAAT  
 GTTCAATAAGAGGAGAGCAAAATATCTTGTTTAAAGGAAATCGGAGCAGTACAAAAACG  
 40 GTCTTACAAGTAGCAAAATCTATAAATTTATGTTCTAATACGCGCAATTTCTAGTCAAT  
 AAAAAGGTCAAAAAATGAGCTGGATTAAACGAATTTTAGTAAAAGTCCTTCTCTCCA  
 CTCGAAAAGCCAAATGTGCCAGAGGCGTATGGACAAAATGTACTGCTTGTGAACAAGTAC  
 TTTATAGTGAAGAACTCAAACGTAATCTGTATGTTTCCCGAAATGTGGTCATCATATGC  
 GTATTGATGCTCGTGAGCGTTTATTAAATTTATTGGACGAAGATTCAAGCCAAAGAAATG  
 45 CGGCAGATTTAGAACCAAAAGATATTTTAAATTCAAAGATTAAAGAAATATAAAGATC  
 GTATCAATGCGGCCCAAAAGAACGGGCGAGAAAGATGCGCTAATTACTATGACAGGTA  
 CACTTATAATATGCAATCGTTGTGGCTGCATCGAATTTGCTTTTATGGGCGGTTCAA  
 TGGGTTCTGTAGTTGGTGCAAAATTTGTTAAAGCGGCTGAAAAGCGATGGAATGAATT  
 GTCCATTTGTGTGTTCTCTGCGAGTGGTGGTCTCGTATGACGGAAGCATTATCTCTT  
 50 TAATGCAAAATGGCAAAATAGTGCCGTAATGCTCAAAATGCGTGAAAAGGGGTGCCAT  
 TTATTTCAATATTACGGATCCGACTTTAGGCGGCGTATCAGCCAGTTTTCGATGTTAG  
 GGGATTTAAATATTGCCGAGCCAAAGCCTTAATGGTTTTGCAGGGCCACGCGTTATTG  
 AACAACTGTGCGTGAAAAATGGCAGAAAGGTTCCAACGTAGTGAGTTTCTACTTGAGA  
 55 AAGGGCAATTGATATGATCGTGAACGTTTCAGAAATGCGT

SEQ. ID NO:67

Nucleotide sequence of DNA region (1000 bp ) up-stream from the P5 gene from  
*Haemophilus influenzae* (HiRd)

TCACTTAATTCAAGCGCATCAATGTTTTCTAAACATCAACAGAATTGACCGCACTTGTA  
 TCTAAAATTTCCGCATTTATTAAGACTGCGCGTAATGCCAAACATGATTAGAGGTTTTA  
 CCATATTGCAATGAGCCTTGCCCGAGGCATCGGTGTTAATCATTCCACCTAAAGTCGCT  
 CGATTGCTGGTGGACAGTTCTGGGGCAAGAAACAAACCATGTGGTTTTAAATGATTGA  
 AGTTGATCTTTTACTACGCTGCTTGACTCGAACCAACGTTCTTTTACATTGAGTTCT  
 AAGATGGCTGTATATGACGAGAAAGATCCACTATTATATTGTTATTGATGGATTGCCCA  
 65 TTTGTGCCAGTGCCCTCCACCGCGAGGCGTAAAGCTGATTGATTGATATTCAAGTAAATTT  
 GCCAATTTTGTATCCGCACTATATCAGCAACCGTTTTTCGGAAGAAAGAAATGCTTGTGGA  
 AGTTGTTGGTAAACGCTGTTATCCGTAGCCAGACTTAATCTATCTGCATAGTTTGTGCGA  
 ATATCCCCCTCAAAATGTTGGCATTGAAGATCATCAAGATAATCAAGTACATATTGTTCA  
 ACTTGAGGAATGCGATTTAGATTGGCAACATAGTATTGACCCATTTAAACATATCAGA  
 70 TGGAGGCTTTGATAATATCCTAAGGCTAGAATAATGTCGATTAGGAAAGAGAGAGGAGAA  
 AGTAAAAAGTCTGTTTAAAGAAAGTGTATTTTGGATAAAAACTAAACAAAAAATCAAAA  
 GAATTTGATCTTTCAATTTTATAGGATAATAAGCGCACTTTTGAACGTTCCCTTTGGGG  
 TAAACATAAGCAAAGGAATTGAATTTGTCAAAAGGTAATAAAGTAGGGCAAAATCAAAAC  
 CCTAGTTAAGTGACTGTTTATAATGTAGCTTTAATTAAGTTTCAGTATAAACAAAGGACA  
 75 CTTTTTATTACTATTTCGATCACTAAATAGAGGACATCAAAA

SEQ. ID NO:68

Nucleotide sequence of DNA region (1000 bp ) up-stream from the D15 gene from *Haemophilus influenzae* (HiRd)

5 TCGATTGTATCCTATATAAATTATAGACGTAAAAATCATTAAATAATGCAAAACACCGTT  
AAGCTTAATAACAGTGCTGCGCCAATTTCGATAACAGATGCTTTCACCCGCTCAGAAACA  
GGTTTTCCTTTAACAGCTTCCATTGTAAAAAACTAAATGACCGCCATCTAATACTGGT  
AATGGAATAAATTCATAATCCCTAAATTTACACTAATCAATGCCATAAACTTAAAAAA  
TACACCAATCCAATATTGCTGATGCGCCAGCACCTTTTGCAATAGAAATGGCCCACTT  
10 AAATTATTTAATGACAAATCGCCAGTAAGTAATTTCCCTAATATTTTCAAGGTTAAAGG  
GAAAGCTGTCTGTTTTTCAATGCCTTTTGTAAAGATTCAAGAATACCATATTTTAAAT  
TCAGTACGGTATTCATCCGCTAATTTGTAAAGGCTGGGCTAACCCCAACAAACCATTTG  
CCATTTTGATTACGCACTGGAGTTAGGACTTTGTCAAATGTTTCTCCATTACGTTCAACT  
TTAATAGAAAAGATTGCGCTTGTTCGACCTGTTTTATAAAATCTTGCCAAGGAAGTCCG  
15 GTTAAATTTTCTTTTAAAAATTTATCACCAGTTTGTAAACCAGCTTCTCAGCGGGAGAA  
TTTTGAACAACCTTAGAAAGCACCATTTCATTTTAGGACGCATAGGCATAATCCCTAAT  
GCCTCAAAGCACTTTCTTTTTCAGGATCGAATGTCCAATTTGTAAAGTTTAAAGTCCGT  
TGTGTGTTCAATATTAGAATTGAAAGGAGAAGGCTAATCTCAACATTAGGCTCCCCATT  
TTTGTGGCAAGTAGCATATTGATGGTTTCCCAATCTTGAGTTTCTTCGCCATCAATTGTA  
20 AGAATTTGCGTATTGGGTTCAATGTGGGCTTGTGCTGCGATTGAGTTTGGTGTATTGAT  
TCAATCACTGGTTTAAACCGTTGGCATTCATAAAGGTAAT

SEQ. ID NO:69

Nucleotide sequence of DNA region (1000 bp ) up-stream from the Omp26 gene from *Haemophilus influenzae* (HiRd)

25 TTTGATAAATACCTTAATTAATGATGGGTTTAATATTTCTCTGCCCAATTAAATTAG  
GCAGAGAACGTTGTTTTGAGTTCTGATGAAGAAAAAGTTCAATTTATTAGAAAGAAC  
TCCAATACTAATTTGGAACCTGTTGACATCATCTTTTCATATTTTAAATTGGTTGGC  
ATAAGAGAATACCAATGGCCCAATAGGAGATTGCCATTGGAATCCGACACCTGTAGAGGC  
30 CGGAATACGGCTTGATTGCTTATGCGCATATCGGGTAAGCTTTTAAATACATTGTTATCAACC  
ACTCTTATCCGATTTCACCTTAGTATTCCAAACACTTGCCGCATCAACAAATAGGGAGGT  
TCGGACTGTATTTGGCTTTTATCACTCAGAAACGGTGTGGTACAATAAGTTCTGCACT  
CGCAGTTGTGATTGCTATACCAATCAGATCAGAACTTATCTCTTAAAGTACCATT  
35 ACCATTACCATTGTTCTGCATAAATTGCGTTAGGTCCAATACTACCATAAGCAAAACCAG  
TAATGAACCGGATGCCACCCGCTGTATAAGTTTGATAGAACGGTAAACGCTTGTTCCTAAA  
ACCATTGCAATATCCGTCAGATGCTTTTGCAGATACAAACCCAGAGGTGATCTCTGTCTAA  
TGGGTAGAAACCTGTACGCTGCACTTAGTTGTAGTATTTGTTATCAGAACCTGGAAT  
AGTAACCTCGTCCCAAGACTTGCTTTAACCCCTTAGTTGGGAAATAGCCTCTATTAG  
40 GCTGTTGATTTCCCAACCAAGAAAAATCAAAGTCATTGTTTAAAGCCATTACCTTT  
AAATTTCAATTGATTGAATATATAAATTACGGTTATATTCTAGAGCAAGTTACTAATTTT  
ATTATAGGTATGGCTAATCTACATAATAGGAGTTATTTTCATTTACAGGGAAACCTAA  
AGTAACATTACTTCCATAAGTCGTACGCTTATAGTTAGAGG

SEQ. ID NO:70

Nucleotide sequence of DNA region (1000 bp ) up-stream from the P6 gene from *Haemophilus influenzae* (HiRd)

45 TTAGATTTCCTCTAAATGAGTTTTTATTTAGTTAAGTATGGAGACCAAGCTGGAAATTT  
AAGTTGACCATCACTTCTTGAAGGCTCGCCTTAAAGCGACCATCTGCGGAAACCAATTG  
TAGCACCTTTCTTAAGCCCTGTGTAGAACTATAAATAATCATAATTCATTGAGAGAG  
50 GCTTGGGCTTTGCGCTAGAAAAGATGTAAGTACCTCTGAAACGCCGTTGTGAGATC  
TTGTTTAACATCATTATTGTTACCATTAATCATCACAAGTGTTTTCCATCTGCACTAAT  
TTGTGCGCTACCGGACCACTGCTGTTGCACTACCAACCGGTTGCATCCATTGATA  
AACTTGTGGCGAACCACTTCTATCGGATGTAAATAAATTTGAATTTCCGCTCTGGCGACCA  
55 CGCTGGTTCAGTATTATTACCGCACCACTCGTCAATTGAGTAGGTGTACCGCCATTGTC  
TCCCATACGTAATATTTCAGAACACCATCAGAGAAAGCAAAAGCTAAACGAGAACCC  
ATCTGGCGAAAAGGCTGGTGCCTTATGCCCTTGAAAAGATGCCACTACTTTACGTGC  
GCCAGAAATTTAAATCCTGTACAAACAAGTTGTGATTTTTTATTTTCAAACGATACATAAGC  
CAACAGCTGGCCGCTCTGGAGACCAAGCTGGAGACATAATTGGTTGGGCACTACGATTGAC  
60 GATAAATTGATTATAGCCATCATAATCTGCTACACGAACCTCATAAGGTTGCGAACCGCC  
ATTTTTTGCACAACATAAGCGATACGAGTTCTAAAGGCACCAAGGATCGCAGTTAATTT  
TTCAAAACCTTCATCGCTCACAGTATGCGCGCCATAGCGTAACCATTTATTTGTTACTGT  
ATAGCTATTTTGCATTAAATACAGTCCCTGGCGTACCTGATGCACCAACCGTATCAATTAA  
TTGATAAGTAATACTATAACCATTACCCGATGGAACCACTT

SEQ. ID NO:71

Nucleotide sequence of DNA region (1000 bp ) up-stream from the TbpA gene from *Haemophilus influenzae* (non-typeable)

70 GGCGATAACCGAGTTTTTGGGGTATTTAGTGCCAAAGAAGACCCACAAAACCCAAATTA  
TCCAGAGAAACCTTAATTGATGGCAAGCTAAGTACTTTTAAAGAACTGATGCAAAACCC  
AATACAACAGCCGATACAAACAACCAATAAAACAACCAATGCAATAACCGATGAAAAAAC  
TTTAAGACCGGAAGATATACTAAGTTTTTGGTGAAGCTGATTATCTTTTAAATGACAATCAG  
CCTGTTCCGCTTTTACCTGAAAAAAATACTGATGATTTTATAAGTAGTAGGCATCATACT  
GTAGGAAATAAACGCTATAAAGTGGAAGCATGTTGCAAGAATCTAAGCTATGTAAATTT

GGTATGTATTATGAAGACCCACTTAAAGAAGAAGAAAAAGAAAAAGAAAAAGAC  
 CAAGAAAAAAGAAAAAGAAAAACAAACGACGACAACTCTATCGAGACTTATTATCAA  
 TTCTTTAGGTACCGTACTGCCAAGGCCGACATACCTGCAACGGGAAACGTGAAATAT  
 5 CGCGGTAATTGGTTTGGTTATATTGGTGATGACACGACATCTTACTCCACTACTGGAGAT  
 AAAAAAGCTCTCGCCGAGTTTGATGTAAATTTTGGCGATAAAAAAGCTAACAGCGGAATTA  
 AACGCACACGATAATGGAAATACCGTATTTAAATTTACTGCAGACCTTCAAAGTGGTAAG  
 AATGACTTCACTGGTACAGCAACCGCAACAAATTTTGTAAATAGATGGTAACAATAGTCAA  
 ACTGGAAATACCCAAATTAATATTAACCTGAAAGTAAATGGGGCACTTTTATGGACCTAAG  
 10 GCTACAGAATTAGGCGGTTATTTACCTATAACGGAATTTCTACAGCTAAAAATTCCTCA  
 ACCGTACCTTCACCACCAATTCACCAATGCAAGAGCTGCAGTTGTGTTTGGAGCTAAA  
 AAACAACAAGTAGAACAACCAAGTAATGGAATACTAAAA

SEQ. ID NO:72

Nucleotide sequence of DNA region (1000 bp ) up-stream from the TbpB gene  
 from *Haemophilus influenzae* (HiRd)

15 TAGAATTATATTCTTATACAAAATTGATAATTGTTTCGCATTATCATTTTTTTTTTGTAAAT  
 AATGTCAACTTATAATTTTTTAAGTTCATGGATAAAATATGAAAAATGGCGTAAAAACAC  
 TTTTCTCTTATCATTAAATAGGCTTATCATTACGAATGTAGCTTGGGCAGAGTTGCAC  
 20 GTCCATAAAATGATACATTGACAAATACGATTCAAAGTGGGAATTAAAAACCTCCTCTT  
 TTTCTCTATGCCTAAGAAAGAAATACCAATAGGCATATTATTTCTCTTTCCAAAAGCC  
 AATTAGCGCACCATCCAAGGCTTGTTCGCTGGGTAAATCCTGCTTTATATCAAAAATA  
 ACACTCAGGCAGTTCAACTGTTATTACCACTATATAAACAATTTCTCAACAAGATAATT  
 TCTTACTAAGCTTGGGCAAGGCTATTGAAGCTCGTGAACAAGGTGATTAACTCAATCTA  
 25 TTGCTTAAATTCGTGAATTATTCGCTCGAGACGATCTTACTACCTTTACGTTATTAAAT  
 TAGCTCAAGCTCTATTTTTTAAGTATGAAAATGAAGCTGCCAAAATTCATTTGAAAAAT  
 TACGTACAGAGGTAGATGATGAAAAATTTTAGGTGTTATTGATCAGTATCTTTTAACAC  
 TAAATCAGCGGAATCAATGGATATGGCAAGTAGGATTAATTTTTTAATGATGATAATT  
 TGAATAACGCTCCAAAAGTGGCACAAAATTTGGTAGTTGGACCGCTTGGGAAAAAGAAA  
 30 GTGGGCAGGGGGTAGGGTATTCTTTATCAGTAGAAAAAATGGCCATGGGCAGATCAT  
 TTTTATGATAAACTATGTTTAAATGGGAATGGAAAATATTATTGGGATAATAAAAAATACA  
 ATGAGGCTACTGTGCGTATAGGTGGTGTAGGCTATCAAACTGCCTCAGTTGAAGTCT  
 CGTTGTTCTTTTCAAGAAAAACGCTGGTATGCAGGCGGT

SEQ. ID NO:73

Nucleotide sequence of DNA region (1000 bp ) up-stream from the HifA (pilin)  
 gene from *Haemophilus influenzae* (LKP serotype 1 genome)

35 TAATAAATTGCTCCATAAAGAGGTTTGTGCCTTATAAATAAGGCAATAAAGATTAAATATA  
 AACCGTTTATTAAGTCCAAAGGCTTAATAAAGCAGCAAACTTTGTTTTCCCAAAAAAAG  
 TAAAAAAGCTCTCCATTATATATATATATATATATTAATAAGGCCCTTTTGAATAATTT  
 40 CATATTTTTTTGAATTAATTCGCTGTAGGTTGGGTTTTTGCCACATGGAGACATATAAA  
 AAAGATTTGTAGGGTGGGCGTAAGCCACGCGGAACATCATCAACAAGTGAATGTTGT  
 ATTAGGCACGCTGGGCTTATGCCTCGCCTACGGGAAATGAATAAGGATAAATATGGGCT  
 TAGCCAGTTTATGGATTAATTATGTTGAAATGGGGAACAATGTTAAAAAACACT  
 45 TTTATTTTTTACCGCACTATTTTTTGCCGCACTTTGTGCATTTTACGCAATGCAGATGT  
 GATTATCACTGGCAGAGTGATTATATCCCGCTGGGCAAAAAATGTTATCGTGAAGTT  
 AGAAAAAATGATGATTGCGCAGCATTGGTGCAAGCCTGGATTGATAATGGCAATCCAAA  
 TGCCGATCCAAAATACACCAAAACCCCTTTTGTGATTACCCCGCCTGTTGCTCGAGTGGA  
 AGCGAAATCAGGGCAAGTTTGGCGATTACGTTACAGGCAGCGAGCCTTTACCTGATGA  
 50 TCGCGAAAGCCTCTTTATTTTAAATTTGTTAGATATTCGCGCGAAACCTGATGCGGCATT  
 TCTGGCAAAACACGGCAGCTTTATGCAAATGCCATTGCTCAGCTTGAAGTTGTTTTA  
 TCGCCCTGCGAACTCTCGATGGATTCTCGTGATGCAATGAAAAAGTAGTGTTTAAAGC  
 CACACCTGAAGGGGTGTTGGTGGATAATCAAAACCCCTTATTATGAATACATTGGTTT  
 GTTACATCAAAATAAACCTGCGAAAAATGTCAAAATGGTTG

SEQ. ID NO:73

Nucleotide sequence of DNA region (1000 bp ) up-stream from the HifE (tip  
 pilin) gene from *Haemophilus influenzae* (LKP serotype 1 genome)

55 TAGTAGATTTCCGACGGGCAAAAAATACAATGGTGTTATTTAACCTCACTTTGCCAAATG  
 GCGAGCCAGTGCCATGGCATCCACCGCACAAGATAGCGAAGGGGCATTGTGGGCGATG  
 60 TGGTGCAAGGTGGTGTGCTTTTCGCTAATAAACTTACCCAGCCAAAAGGCGAGTTAATCG  
 TCAAAATGGGTGAGCGAGAAAGCGAACATGCCGTTTCCAATATCAAGTTGATTGGGATA  
 ACGCACAAATACAAAGTCACGATATTCAATGCAAAACCGCAAAATAAATTAATGAAGAGG  
 ATTTATGCAAAAAACACCAAAAAATTAACCGCGCTTTTCCATCAAAAAATCCACTGCTAC  
 65 TTGTAGTGGAGCAAAATATAGTGGAGCAAAATATAGTGGCTCAAAATGCTTTAGGTTTCA  
 TCGTCTGGCTCTGCTTGCTTGCGTGGCTCTGCTTGATTGCATTGTGGCACTGCCTGCTTA  
 TGCTTACGATGGCAGATGACCTTTCAAGGGGAGATTTAAGTGATGGCACTTGTAATAAT  
 TGAACACAGACAGCCAAAATCGCACGGTTACCTTGCCAACAGTGGGAAAAGCTAATTTAAG  
 70 CCACGCAGGGCAACCGCCCGCCCTGTGCTTTTCCATCACGTTAAAAAGAAATGCATGC  
 AGATGATGCTATGAAGCTAATCTGCTATTTAAAGGGGAGACACACACAGGGCAATC  
 TTATCTTTCCAATAAGGCAGGCAACGGCAAGCCACCAACGTGGGCATTCAAAATGTCAA  
 AGCCGATGGCATAGGCAGCCTATCAAGGTGGACGGCACCGAAGCCACAGCGAAAAAGC  
 CCCCACACAGGTAAAGCGCAAAACGGCACAGTTATTAACCCCGTTTTGGCTACTTTGG  
 75 CTCGTTATTACGCCACAGGTGAAGCCACCGCAGGCGACGTTGAAGCCACTGCAACTTTTG  
 AAGTGCAGTATAACTAAAAATTTTATTATCCAGTGAAAAA

## SEQ. ID NO:75

Nucleotide sequence of DNA region (1000 bp ) up-stream from the P2 gene from *Haemophilus influenzae* (HiRd)

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5 1 TTATCCGCTA ACATTTTCATC AGTAATTCCA TGAACCTTAA TCGCATCAGG
51 ATCANCAGGGG CGATCTGGCT TAATATAAAT ATGAYAATTA TTACCTGTGT
101 AACGACGATT TATTAATTCA ACTGCACCAA TTTCAATAAT GCAGTGTCCCT
151 TCATAATGCG CGCCAAGCTG ATTCATACCT GTAGTTTCAG TATCTAATAC
201 AATTGGCGGA TTGGGATTAA TCATTGTGTC AACCTATCTC TTTCCATTAA
251 AATACTTGCC ATTCTACACA ACAACCTTTT TGTATGCKK AAACAGATTG
10 301 AAATTTTAC TGATGGATCT TGCTTAGGTA ATCCAGGGGC GGGCGGAATT
351 GGTGCCGTAT TGCGTTATAA ACAACATGAA AAAACACTCT CCAAAGGCTA
401 TTTCCAAACC ACCAATAATC GAATGGAATT ACGCGCTGTC ATTGAAGCAT
451 TAAATACATT AAAAGAACCT TGCTTGATCA CGCTTTATAG TGATAGCCAA
501 TATATGAAAA ATGGCATAAC CAAATGGATC TTTAACTGGA AAAAAAATAA
15 551 TTGGAAAGCA AGTCTGGAA AGCCTGTAAA AAACCAAGAT TTATGGATAG
601 CCTTAGATGA ATCCATCCAA CGTCATAAAA TTAATTGGCA ATGGGTAAAA
651 GGCCATGCTG GACACAGAGA AAATGAAATT TGGATGAAT TAGCAAAAAA
701 AGGGGCAGAA AATCCGACAT TGGGAAGATAT GGGGTACATA GAAGAATAAT
751 ACAACTGATA TACCGTCATA TTTTTCGATA CCTAAAAATA TTTAATACTT
20 801 AAACCTAAAA CAGAATAAAA AATAATCAAA TTCATTTAAA AAATGTGATC
851 TCGATCAGAT TTCAAGAAAA TTTAAATTTT GGAGTATTGA CATCAAAAAAT
901 TTTTGTGTA AAGATGCAGC TCGTCCGTTT TGGCGATTGG ACAATTCTAT
951 TGGAGAAAAG TTCAATCATA GATAGTAAAC AACCATAAGG AATACAAATT
1001 A
25

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## SEQ. ID NO:76

Nucleotide sequence of DNA coding region (partial) of the *Moraxella Catarrhalis* HtrB gene

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30 1 TCAGTGTCTG GTTTTTAAAG ATATGTACCG CTGTCAGTCC TGCATGGATT
51 GGGCGCGTGT GCGTCTTATA TTTCTATCA TTGCAGGCTT AGTATTTATC
101 GCAGCATCCA AGCCAAATTTA ATCTTGGTTC ACCCCAAGAT GCCAGACGCA
151 CAGCGGCAAA AACTCGCCAA ACAATCCTA AAAAATCAGC TCATCAGTGC
201 AGTCGACAGT CTTAAAACCT GGGCAATGCC ACCAAAATGG TCTATCGCAC
251 AAATTAAAC GGTTCATCAT GAAGATATCC TAATCAAAGC ACTTGCCAAAT
35 301 CCAAGTGGTA TGCTTGCCAT TGTGCTCAT ATCGGCACTT GGGAGATGAT
351 GAATGCTTGG CTCATACCT TTGGCTCCCC TACTATCATG TATAAGCCCA
401 TCAAAAATGC GCGGTTAGAT CGCTTTGTTT TACAGGGGCG TGAAAGACTA
451 AATGCCAGCC TTGTACCCAC AGATGCTAGT GGTGTTAAGG CAATTTTTAA
501 AACACTCAAA GCAGGTGGAT TTAGTATCAT ACTGCCCGAC CATGTACCTG
40 551 ATCCATCAGG TGGTGAGATT GCTCCTTTTT TTGGTATTAA AACCTTAACC
601 AGTACGCTGG CGTCAAAGCT TGCTGCAAAA ACTGGTTGTG CTCTTGTTGG
651 CTTAAGCTGT ATTCGGCGTG AAGATGGCGA TGGTTTTGAA ATTTTGTGTT
701 ATGAATTAAA TGATGAACAA CTTTATTCAA AAAATACCAA AATTGCAACC
751 ACTGCTTTAA ATGGTGCGAT GGAACAAATG ATTTATCCAC ATTTTGTGCA
45 801 TTATATGTGG AGCTATCGTC GGTTCAGCA TACACCACTA TTAAATAATC
851 CTTATTTACT TAATGAAAT GAGCTAAAAA AAATAGCCAT AAAGCTTCAA
901 GCCATGTCAA AGGATAGTTA TGAG

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Protein Seq: 25% identity and 35% similarity with HtrB from *E. coli*

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50 1 SVLGFLRYVF LSVLHGLAAC ASYISYHCR LSIYSIQANL ILVHPKMPDA
51 QRQKLAKQIL KNQLISAVDS LKTWAMPPKW SIAQIKTVHH EDILIKALAN
101 PSGMLAIVPH IGTWEMMNAW LNTFGSPTIM YKPIKNAVD RFVLQGRERL
151 NASLVPTDAS GVKAIKFTLK AGGFSIILPD HVPDPSSGGEI APFFGIKTLT
201 STLASKLAAK TGCALVGLSC IRREDGDGFE IFCYELNDEQ LYSKNTKIAT
55 251 TALNGAMEQM IYPHFLHYMW SYRRFKHTPL LNNPYLLNEN ELKKIAIKLQ
301 AMSKDSYE

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## SEQ. ID NO:77

Nucleotide sequence of DNA coding region of the *Neisseria* (meningococcus B) HtrB gene

```

60 1 ATGTTTCGTT TACAATTCGG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51 CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGTGTC CCACTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
65 151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAACAGTCA AAGCCGTTT TCGGGAACG GCAAAAGGCG
251 GTTTGGAATC TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGTT
70 401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAATAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGCAAGCAA CCATCGTCCT GCCCGACCAC

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601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG  
 651 CAAACCTGCG TATACCATGA CGCTGGCGGC AAAATTGGCA CAGTCAAAG  
 701 GCGTGAAGAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT  
 751 TTCGATTGCG ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC  
 801 CCAATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT  
 851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCG

**Protein Sequence - 30% identity and 38% similarity with Htrb *E. coli***

1 MFRLLQFLFP PLRTAMHILL TALLKCLSLP PLSCLHTLGN RLGLHAFYLL  
 51 KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDLET  
 101 MFKAHVHWEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLFFPLTAMY  
 151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIKALRS GEATVLPDH  
 201 VSPQEGGEG VWVDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG  
 251 FDLHIRPVQG ELNGDKAHD AVFNRAEYV IRRFPTQYLF MYNRYKMP

**SEQ. ID NO:78**

**Nucleotide sequence of DNA coding region of the *Haemophilus influenzae* (non-typeable) HtrB gene**

1 ATGAAAAACG AAAAAGCTCC TCAATTTCAA CCGCACTTTT TAGCCCCAAA  
 51 ATACTGGCTT TTTTGGCTAG GCGTGGCAAT TTGGCGAAGT ATTTTATGTC  
 101 TTCCCTATCC TATTTTGGCG CATATTGGTC ATGGTTTCGG TTGGCTGTTT  
 151 TCACATTTAA AAGTGGGTAA ACGTCGAGCT GCCATTGCAC GCCGTAATCT  
 201 TGAACCTTGT TTCCCTGATA TGCTGAAAA CGAACGTGAG ACGATTTTGC  
 251 AAGAAAAATCT TCGTTCAGTA GGCATGGCAA TTATCGAAAC TGGCATGGCT  
 301 TGGTTTTGGT CGGATTCACG TATCAAAAAA TGGTCGAAAG TTGAAGGCTT  
 351 ACATTATCTA AAAGAAAATC AAAAAGATGG AATTGTTCTC GTCGGTGTTC  
 401 ATTTCTTAAC GCTAGAACTT GGCGCACGCA TCATTGGTTT ACATCATCCT  
 451 GGCATTGGTG TTTATCGTCC AAATGATAAT CCTTTGCTTG ATTTGGCTACA  
 501 AACACAAGGC CGTTTACGCT CCAATAAAGA TATGCTTGAT CGTAAAGATT  
 551 TACGCGGAAT GATCAAAGCT TTACGCCACG AAGAAACCAT TTGGTATGCG  
 601 CCTGATCAGC ATTACGGCAG AAAAAATGCC GTTTTGTGTC CTTTTTTTGC  
 651 AGTACCTGAC ACTTGCACCTA CTACTGGTAG TTATTATTTA TTGAAATCCT  
 701 CGCAAAACAG CAAAGTGATT CCATTTCGCG CATTACGCAA TAAAGATGGT  
 751 TCAGGTGATA CCGTGAGTAT TTCAGCGCCT GTTGATTTTA CGGATTTACA  
 801 AGATGAAACG CGGATTGCTG CGCGAATGAA TCAAATCGTA GAAAGGAAA  
 851 TCATGAAGGG CATATCACA TATATGTGGC TACATCGCCG TTTTAAACAA  
 901 CGTCCAGATG AAAATACGCC TAGTTTATAC GATTAA

**Protein Sequence - 57% identity and 66% similarity with HtrB *E. coli***

1 MKNEKLPPQF PHFLAPKYWL FWLGVAIWS ILCLPYPIRL HIGHGFGWLF  
 51 SHLKVGKRRR AIARRNLELC FPDMPENERE TILQENLRV GMALLETGMA  
 101 WFWSDSRICK WSKVEGLHYL KENQKDGIVL VGVHFLTLEL GARIIGLHHP  
 151 GIGVYRPNDN PLLDWLQTOG RLRSNKDMLD RKDLRGMKA LRHEETIWA  
 201 PDHGYGRKNA VVPPFAVPD TCTTTGSYYL LKSSQNSKVI PFAPLRNKDG  
 251 SGYTVSISAP VDFTDLQDET AIAARMNQIV EKEIMKGISQ YMWLHRRFKT  
 301 RPDENTPSLY D\*

**SEQ. ID NO:79**

**Nucleotide sequence of DNA coding region of the *Haemophilus influenzae* (non-typeable) MsbB gene**

1 ATGTCGGATA ATCAACAAAA TTTACGTTTG ACGGCGAGAG TGGGCTATGA  
 51 AGCGCACTTT TCATGGTCGT ATTTAAAGCC TCAATATTGG GGGATTTGGC  
 101 TTGGTATTTT CTTTTTATTG TTGTTAGCAT TTGTGCCTTT TCGTCTGCGC  
 151 GATAAATTGA CGGAAAAATT AGGTATTGTT ATTGGGCATA AAGCAAAGAA  
 201 ACAGCGTACG CGTGCACAAA CTAACCTTGA ATATTGTTTC CCTCATTGGA  
 251 CTGAACAACA ACGTGAGCAA GTGATTGATA AAATGTTTGC GGTGTGCGCT  
 301 CAGGTTATGT TTGGTATTGG TGAGATTGCC ATCCGTTCAA AGAAACATTT  
 351 GCAAAAACGC AGCGAATTTA TCGGTCTTGA ACATATCGAA CAGGCAAAAG  
 401 CTGAAGGAAA GAATATTATT CTTATGGTGC CACATGGCTG GCGGATTGAT  
 451 GCGTCTGGCA TTATTTTGCA CACTCAAGGC ATGCCAATGA CTTCTATGTA  
 501 TAATCCACAC CGTAATCCAT TGGTGGATTG GCTTTGGACG ATTACACGCC  
 551 AACGTTTCGG CGGAAAAATG CATGCACGCC AAAATGGTAT TAAACCTTTT  
 601 TTAAGTCATG TTCGTAAGG CGAAATGGGT TATTACTTAC CCGATGAAGA  
 651 TTTTGGGGCG GAACAAAGCG TATTGTGTA TTTCTTTGGG ACTTATAAAG  
 701 CGACATTACC AGGGTTAAAT AAAATGGCAA AACTTTCTAA AGCCGTTGTT  
 751 ATTCCTAATG TTCTCTGTTA TAACGCTGAA ACGGGCAAAT ATGAAATGGA  
 801 AATTCAATCT GCAATGAATT TAAGTGATGA TCCTGAACAA TCAGCCCGAG  
 851 CAATGAACGA AGAAATAGAA TCTTTTGTTA CGCCAGCGCC AGAGCAATAT  
 901 GTTTGGATT TCGAATTATT GCGTACAAGG AAAGATGGCG AAGATCTTTA  
 951 TGATTAA

**Protein Sequence - 45% identity and 56% similarity with MsbB *E. coli***

1 MSDNQONRLR TARVGYEAF SWSYLKPQYW GIWLGIFLL LLAFFVPRLR  
 51 DKLTKGLGIW IGHKAKKQRT RAQTNLQYCF PHWTEQQREQ VIDKMFVAVD  
 101 QVMFGIGEIA IRSKKHLQKR SEFIGLEHIE QAKAEGKNII LMVPHGWAI  
 151 ASGIILHTQG MPMTSMYNPH RNPLVDWLWT ITRQRFEGKM HARQNGIKPF

201 LSHVRKGMG YYLPDEDFGA EQSVFVDFG TYKATLPGLN KMAKLSKAVV  
 251 IMFPPRYNAE TGKYEMEIHP AMNLSDDPEQ SARAMEEIE SFVTPAPEQY  
 301 VWILQLLRTR KDGEDLYD\*

## 5 SEQ. ID NO:80

**Nucleotide sequence of DNA coding region of the *Moraxella catarrhalis* MsbB gene**

1 ATGAGTTGCC ATCATCAGCA TAAGCAGACA CCCAAACACG CCATATCCAT  
 51 TAAGCATATG CCAAGCTTGA CAGATACTCA TAAACAAAGT AGCCAAGCTG  
 101 AGCCAAAATC GTTTGAATGG GCGTTTTTAC ATCCCAAATA TTGGGGAGTT  
 151 TGGCTGGCTT TTGCGTTGAT TTTACCGCTG ATTTTCTAC CGCTGCGTTG  
 201 GCAGTTTGG ATCGGCAAGC GTCTTGGCAT TTTGGTACAT TACTTAGCTA  
 251 AAAGCCGAGT TCAAGACACT CTAACCAACC TGCAGTTTAC CTTCCCAAAT  
 301 CAACCAAAT CAAAACACAA GGCCACCGCA CGGCAAGTAT TTATTAATCA  
 15 351 AGGTATTGGT ATTTTGAAA GTTTATGTGC ATGGTTTCGC CCTAATGTCT  
 401 TTAACGCAC TTTTAGCATT TCTGGTTTAC AGCATTGTAT TGATGCCCAA  
 451 AAACAAAATA AAGCGGTGAT TTTACTTGGT GGACATCGCA CGACGCTTGA  
 501 TTTGGGCGGT CGGTTATGTA CACAGTTTTT TCGGCGCGAC TCGGTGTATC  
 551 GCCCACAAAA CAACCCTTTG CTTGAATGGT TTATCTATAA TGCACGCCGC  
 20 601 TCCATCTTTG ATGAGCAAAT CTCAAATCGT GATATGAAAA AACTCATCAC  
 651 TCGGCTCAAA CAAGGTCGGA TAATTTGGTA TTCACCTGAT CAAGATTTTG  
 701 GTCTTGAGCA TGGCGTGATG GCGACCTTTT TTGGTGTGCC TGCAGCAACG  
 751 ATTACCGCTC AGCGTCGTCT TATTAAGCTG GGTGATAAAG CCAATCCTCC  
 801 TGTTCATCAT ATGATGGATA TGCTCAGACA AACGCCCGAT TATATCGCAA  
 25 851 AAGGTCACCG TCCACATTAT CACATCAGCC TAAGCGCTGT GTTAAAAAAT  
 901 TATCCAGCG ATGACGAAAC CGCCGATGCT GAACGCATCA ATCGACTGAT  
 951 TGAGCAAAT ATTCAAAAG ATTTAACCCA GTGGATGTGG TTTTCATCGCC  
 1001 GCTTTAAAC TCAAGCCGAT GACACCAATT ACTATCAACA TTAATG

30 Protein Sequence - 28% identity and 37 similarity with MsbB of *E. coli*

1 MSCHHQHKQT PKHAISIKHM PSLTDTHKQS SQAEPKSEFW AFLHPKYWGV  
 51 WLAFAFALPL IFPLRWQFW IGKRLGILVH YLAKSRVQDT LTNLQLTFPN  
 101 QPKSKHKATA RQVFINGGIG IFESLCAWFR PNVEKRTFSI SGLQLHIDAQ  
 151 KQNKAVILLG GHRTTLDLGG RLCTOFFAAD CVYRPQNNPL LEWFIYNARR  
 35 201 CIFDEQISNR DMKKLITRLK QGRIIWYSPD QDFGLEHGMV ATFFGVPAAT  
 251 ITAQRRLIKL GDKANPPVII MMDMLRQTPD YIAKGHRPHY HISLSAVLKN  
 301 YPSDDETADA ERINRLIEQN IQKDLTQWMW FHRREKTQAD DTNYVQH\*

## SEQ. ID NO:81

**Nucleotide sequence of DNA coding region of the *Neisseria* (meningococcus B) MsbB gene**

1 ATGAAATTTA TATTTTTGT ACTGTATGTT TTGCAGTTTC TGCCGTTTGC  
 51 GCTGCTGCAC AAACCTGCGG ACCTGACGGG TTTGCTCGCC TACCTTTTGG  
 101 TCAAACCCCG CCGCCGTATC GGCGAAATCA ATTTGGCAAA ATGCTTTCCC  
 45 151 GAGTGGGACG GAAAAAGCG CGAAACCGTA TTGAAGCAGC ATTTCAAACA  
 201 TATGGCGAAA CTGATGCTTG AATACGGCTT ATATTGGTAC GCGCCTGCCG  
 251 GCGCTTTGAA ATCGCTGGTG CGTTACCGCA ATAAGCATT TTTGGACGAC  
 301 GCGCTGGCGG CGGGGGAAAA AGTCATCATT CTGTACCGCG ACTTCACCGC  
 351 GTTCGAGATG GCGGTGTACG CGCTTAATCA GGATGTACCG CTGATCAGTA  
 50 401 TGTATTCCCA CCAAAAAAAC AAGATATTGG ACGCACAGAT TTTGAAAGGC  
 451 CGCAACCGCT ACGACAATGT CTTCTTATC GGGCGCACCG AAGGCGTGCG  
 501 CGCCCTCGTC AAACAGTTCC GCAAAAGCAG CGCGCCGTTT CTGTATCTGC  
 55 551 CCGATCAGGA TTTGCGACGC AACGATTCGG TTTTGTGGA TTTTTCGGT  
 601 ATTCAGACGG CAACGATTAC CGGCTTGAGC CGCATTGCCG CGCTTGCAAA  
 651 TGCAAAAGT ATACCCGCCA TCCCGTCCG CGAGGCGGAC AATACGGTTA  
 701 CATTGCATT CTACCCGGCT TGGGAATCCT TTCCGAGTGA AGATGCGCAG  
 751 KCCGACGCGC AGCGCATGAA CCGTTTTATC GAGGAACCGT GCGCGAACAT  
 801 CCCGAGCAGT ATTTTGGCT GCACAAGCGT TTCAAACCC GTCCGGAAGG  
 851 CAGCCCCGAT TTTACTGAT ACGTAA

60 Protein Sequence - 25% identity and 36% identity with MsbB *E. coli*

1 MKFIFVLYV LQFLPFALLH KLADLTGLLA YLLVKPRRRI GEINLAKCFP  
 51 EWDGKKRET V LKQHFHMAK LMLEYGLYVY APAGRLKSLV RYRNKHYLDD  
 101 ALAAGEKVII LYPHFTAFEM AVYALNQDVP LISMYSHQKN KILDAQILKG  
 65 151 RNRVDMVFLI GRTEGVRALV KQFRKSSAPF LYLDPQDFGR NDSVFDVDFG  
 201 IQTATITGLS RIAALANAKV IPAIPVREAD NTVTLHFYPA WESFPSEDAQ  
 251 ADAQRMNRFI EEPKANIPSS IFGCTSVSKP VRKAAPIFTD T\*



**We Claim:**

1. A genetically-engineered bleb preparation from a Gram-negative bacterial strain characterized in that said preparation is obtainable by employing one or more processes selected from the following group:
- a) a process of reducing immunodominant variable or non-protective antigens within the bleb preparation comprising the steps of determining the identity of such antigen, engineering a bacterial strain to produce less or none of said antigen, and making blebs from said strain;
  - b) a process of upregulating expression of protective OMP antigens within the bleb preparation comprising the steps of identifying such antigen, engineering a bacterial strain so as to introduce a stronger promoter sequence upstream of a gene encoding said antigen such that said gene is expressed at a level higher than in the non-modified bleb, and making blebs from said strain;
  - c) a process of upregulating expression of conditionally-expressed, protective OMP antigens within the bleb preparation comprising the steps of identifying such an antigen, engineering a bacterial strain so as to remove the repressive control mechanisms of its expression, and making blebs from said strain;
  - d) a process of modifying lipid A portion of bacterial LPS within the bleb preparation, comprising the steps of identifying a gene involved in rendering the lipid A portion of LPS toxic, engineering a bacterial strain so as to reduce or switch off expression of said gene, and making blebs from said strain;
  - e) a process of modifying lipid A portion of bacterial LPS within the bleb preparation, comprising the steps of identifying a gene involved in rendering the lipid A portion of LPS less toxic, engineering a bacterial strain so as to introduce a stronger promoter sequence upstream of said gene such that said gene is expressed at a level higher than in the non-modified bleb, and making blebs from said strain;

- 5 f) a process of reducing lipid A toxicity within the bleb preparation and increasing the levels of protective antigens, comprising the steps of engineering the chromosome of a bacterial strain to incorporate a gene encoding a Polymyxin A peptide, or a derivative or analogue thereof, fused to a protective antigen, and making blebs from said strain; or
- g) a process of creating conserved OMP antigens on the bleb preparation comprising the steps of identifying such antigen, engineering a bacterial strain so as to delete variable regions of a gene encoding said antigen, and making blebs from said strain.

10

2. The genetically-engineered bleb preparation of Claim 1, wherein said preparation is obtainable by employing one or more further processes selected from the following group:

- 15 h) a process of reducing expression within the bleb preparation of an antigen which shares a structural similarity with a human structure and may be capable of inducing an auto-immune response in humans, comprising the steps of identifying a gene involved in the biosynthesis of the antigen, engineering a bacterial strain so as to reduce or switch off expression of said gene, and making blebs from said strain; or
- 20 i) a process of upregulating expression of protective OMP antigens within the bleb preparation comprising the steps of identifying such antigen, engineering a bacterial strain so as to introduce into the chromosome one or more further copies of a gene encoding said antigen controlled by a heterologous, stronger promoter sequence, and making blebs from said strain.
- 25

3. The bleb preparation of claim 1 or 2, wherein the engineering steps of processes a), b), c), d), e), h) and i) are carried out by homologous recombination events between a sequence of at least 30 nucleotides on the bacterial chromosome, and a sequence of at least 30 nucleotides on a vector transformed within the strain.

30

4. The bleb preparation of claim 3, wherein the engineering steps are carried out by double cross-over homologous recombination events between two sequences of at least 30 nucleotides on the bacterial chromosome separated by nucleotide sequence 'X', and two sequences of at least 30 nucleotides on a vector transformed within the strain separated by nucleotide sequence 'Y', wherein during the recombination event X and Y are interchanged.
5. The bleb preparation of claim 4, wherein the two nucleotide sequences are of approximately the same length, and wherein the vector is a linear DNA molecule.
6. The bleb preparation of claim 4 or 5, wherein the recombination events of processes a), b), c), d), e) and h) are carried out within the region of the chromosome 1000 bp upstream of the initiation codon of the gene of interest.
7. The bleb preparation of claim 6, wherein for process a), d) or h) nucleotide sequence X comprises part of the promoter region of the gene, and nucleotide sequence Y comprises either a weak promoter region, or no promoter region.
8. The bleb preparation of claim 6, wherein for process b) or e) nucleotide sequence Y comprises a strong promoter region for the bacterium.
9. The bleb preparation of claim 8, wherein nucleotide sequence Y is inserted 200-600 bp upstream of the initiation codon of the gene of interest.
10. The bleb preparation of claim 9, wherein nucleotide sequence Y is inserted approximately 400 bp upstream of the initiation codon of the gene of interest.
11. The bleb preparation of claim 6, wherein for process c) nucleotide sequence X comprises part of the repressive control sequence of the promoter, and nucleotide sequence Y comprises no such sequence.

12. The bleb preparation of claim 4 or 5, wherein the recombination events of processes a), d), and h) are carried out such that nucleotide sequence X comprises part of the coding sequence of the gene of interest.
- 5 13. The bleb preparation of claim 4 or 5, wherein the recombination events of process i) is carried out such that nucleotide sequence Y comprises the further copy of the gene within an expression cassette.
14. The bleb preparation of claims 1-13 isolated from a modified *Neisseria*  
10 *meningitidis* B strain.
15. The bleb preparation of claim 14, obtainable by employing at least process b) and/or i), wherein one or more genes are upregulated from a list comprising: NspA, Hsf-like, Hap, PorA, PorB, OMP85, PilQ, PldA, FrpB, TbpA, TbpB, FrpA, FrpC,  
15 LbpA, LbpB, FhaB, HasR, lipo02, Tbp2 (lipo28), MltA (lipo30), and ctrA.
16. The bleb preparation of claim 14 or 15, obtainable by employing at least process a), wherein one or more genes are downregulated from a list comprising: PorA, PorB, PilC, TbpA, TbpB, LbpA, LbpB, Opa, and Opc.  
20
17. The bleb preparation of claims 14-16, obtainable by employing at least process d), wherein one or more genes are downregulated from a list comprising: htrB, msbB and lpxK.
- 25 18. The bleb preparation of claims 14-17, obtainable by employing at least process e), wherein one or more genes are upregulated from a list comprising: pmrA, pmrB, pmrE, and pmrF.
- 30 19. The bleb preparation of claims 14-18, obtainable by employing at least process c), wherein the repressive control sequence of the promoter is the *fur* operator region of either or both of the TbpB or LbpB genes.

20. The bleb preparation of claims 14-19, obtainable by employing at least process h), wherein one or more genes are downregulated from a list comprising: galE, siaA, siaB, siaC, siaD, ctrA, ctrB, ctrC, and ctrD.
- 5 21. The bleb preparation of claims 1-13 isolated from a modified *Moraxella catarrhalis* strain.
22. The bleb preparation of claim 21, obtainable by employing at least process b) and/or i), wherein one or more genes are upregulated from a list comprising:  
10 OMP106, HasR, PilQ, OMP85, lipo06, lipo10, lipo11, lipo18, P6, ompCD, CopB, D15, OmpLA1, Hly3, LbpA, LbpB, TbpA, TbpB, OmpE, UspA1, UspA2, and Omp21.
23. The bleb preparation of claim 21 or 22, obtainable by employing at least  
15 process a), wherein one or more genes are downregulated from a list comprising: CopB, OMP106, OmpB1, TbpA, TbpB, LbpA, and LbpB.
24. The bleb preparation of claims 21-23, obtainable by employing at least process d), wherein one or more genes are downregulated from a list comprising:  
20 and lpxK.
25. The bleb preparation of claims 21-24, obtainable by employing at least process e), wherein one or more genes are upregulated from a list comprising: pmrA, pmrB, pmrE, and pmrF.  
25
26. The bleb preparation of claims 1-13 isolated from a modified *Haemophilus influenzae* strain.
27. The bleb preparation of claim 26, obtainable by employing at least process b) and/or i), wherein one or more genes are upregulated from a list comprising: D15, P6, TbpA, TbpB, P2, P5, OMP26, HMW1, HMW2, HMW3, HMW4, Hia, Hsf, Hap, Hin47, and Hif.  
30

28. The bleb preparation of claim 26 or 27, obtainable by employing at least process a), wherein one or more genes are downregulated from a list comprising: P2, P5, Hif, IgA1-protease, HgpA, HgpB, HMW1, HMW2, Hxu, TbpA, and TbpB.

5

29. The bleb preparation of claims 26-28, obtainable by employing at least process d), wherein one or more genes are downregulated from a list comprising: htrB, msbB and lpxK.

10 30. The bleb preparation of claims 26-29, obtainable by employing at least process e), wherein one or more genes are upregulated from a list comprising: pmrA, pmrB, pmrE, and pmrF.

15 31. A genetically-engineered bleb preparation from a Gram-negative bacterial strain characterized in that said preparation is obtainable by employing a process comprising the steps of: introducing a heterologous gene, optionally controlled by a strong promoter sequence, into the chromosome by homologous recombination, and making blebs from said strain.

20 32. The bleb preparation of claim 31, wherein the Gram-negative strain is *Neisseria gonorrhoeae*, and the heterologous gene is a protective OMP from *C. trachomatis*.

25 33. The bleb preparation of claim 31, wherein the Gram-negative strain is *Haemophilus influenzae*, and the heterologous gene is a protective OMP from *Moraxella catarrhalis*.

30 34. The bleb preparation of claim 31, wherein the Gram-negative strain is *Moraxella catarrhalis*, and the heterologous gene is a protective OMP from *Haemophilus influenzae*.

35. A vaccine comprising the bleb preparation of claims 1-34 and a pharmaceutically acceptable excipient.
36. A meningococcal vaccine comprising the bleb preparation of claims 14-20 and  
5 one or more plain or conjugated meningococcal capsular polysaccharides selected from the serotypes A, C, Y or W.
37. A meningitis vaccine comprising the preparation of claims 14-20 or the bleb preparation of claim 32, a conjugated *H. influenzae* b capsular polysaccharide, and  
10 one or more plain or conjugated pneumococcal capsular polysaccharides.
38. An otitis media vaccine comprising the bleb preparation of claims 21-25 and one or more plain or conjugated pneumococcal capsular polysaccharides, and one or more antigens that can protect a host against non-typeable *H. influenzae* infection.  
15
39. An otitis media vaccine comprising the bleb preparation of claims 26-30 and one or more plain or conjugated pneumococcal capsular polysaccharides, and one or more antigens that can protect a host against *Moraxella catarrhalis* infection.
40. The otitis media vaccine of claim 38 or 39, wherein the vaccine additionally comprises one or more protein antigens that can protect a host against *Streptococcus pneumoniae* and/or one or more antigens that can protect a host against RSV and/or one or more antigens that can protect a host against influenza virus.  
20
41. A vector suitable for performing the recombination events described in claims 3-34.  
25
42. A modified Gram-negative bacterial strain from which the bleb preparation of claims 1-34 is made.  
30
43. An immuno-protective and non-toxic Gram-negative bleb, ghost, or killed whole cell vaccine suitable for paediatric use.

44. An isolated polynucleotide sequence which hybridises under highly stringent conditions to at least a 30 nucleotide portion of the nucleotides in SEQ ID NO: 2-23, 25, 27-81 or a complementary strand thereof.

5

45. The isolated polynucleotide sequence of claim 44 comprising at least 30 nucleotides.

46. The isolated polynucleotide sequence of claim 45 comprising at least 30 nucleotides of SEQ ID NO: 2-23, 25, 27-81 or a complementary strand thereof.

10

47. Use of the isolated polynucleotide sequence of claims 44-46 in performing a homologous recombination event within 1000 bp upstream of a Gram-negative bacterial chromosomal gene in order to either increase or decrease expression of said gene.

15

48. A process of genetically upregulating expression of a gene within a Gram-negative bacterial strain comprising the steps of: making a vector comprising a strong promoter sequence and a nucleotide sequence of at least 30 nucleotides which is capable of recombination with a sequence of at least 30 nucleotides in the 1000 bp upstream of the gene, transforming a bacterial strain with the vector, and performing a homologous recombination event between the chromosome and the vector to introduce the promoter within 1000 bp upstream of the initiation codon of the gene.

20

49. The process of claim 48, wherein the promoter is introduced within 200-600 bp upstream of the initiation codon of the gene.

25

50. The process of claim 49, wherein the promoter is introduced approximately 400 bp upstream of the initiation codon of the gene.

30

51. The process of claim 48-50, wherein the homologous recombination event is effected through a double cross-over between two sequences of at least 30 nucleotides



on the bacterial chromosome separated by nucleotide sequence 'X', and two sequences of at least 30 nucleotides on the vector separated by nucleotide sequence 'Y' which comprises the strong promoter sequence, wherein the vector is a linear nucleotide sequence, and wherein during the recombination event X and Y are  
5   interchanged.

52.   The process of claim 51, wherein the two nucleotide sequences are of approximately the same length.

10   53.   A modified bacterial strain obtainable by the processes of claims 48-52.

54.   A method to produce a genetically-engineered bleb preparation from a Gram-negative bacterial strain by employing one or more processes selected from the following group:

15       a)    a process of reducing immunodominant variable or non-protective antigens within the bleb preparation comprising the steps of determining the identity of such antigen, engineering a bacterial strain to produce less or none of said antigen, and making blebs from said strain;

      b)    a process of upregulating expression of protective OMP antigens  
20   within the bleb preparation comprising the steps of identifying such antigen, engineering a bacterial strain so as to introduce a stronger promoter sequence upstream of a gene encoding said antigen such that said gene is expressed at a level higher than in the non-modified bleb, and making blebs from said strain;

      c)    a process of upregulating expression of conditionally-expressed,  
25   protective OMP antigens within the bleb preparation comprising the steps of identifying such an antigen, engineering a bacterial strain so as to remove the repressive control mechanisms of its expression, and making blebs from said strain;

      d)    a process of modifying lipid A portion of bacterial LPS within the bleb preparation, comprising the steps of identifying a gene involved in rendering the lipid  
30   A portion of LPS toxic, engineering a bacterial strain so as to reduce or switch off expression of said gene, and making blebs from said strain;

e) a process of modifying lipid A portion of bacterial LPS within the bleb preparation, comprising the steps of identifying a gene involved in rendering the lipid A portion of LPS less toxic, engineering a bacterial strain so as to introduce a stronger promoter sequence upstream of said gene such that said gene is expressed at a level  
5 higher than in the non-modified bleb, and making blebs from said strain;

f) a process of reducing lipid A toxicity within the bleb preparation and increasing the levels of protective antigens, comprising the steps of engineering the chromosome of a bacterial strain to incorporate a gene encoding a Polymyxin A peptide, or a derivative or analogue thereof, fused to a protective antigen, and making  
10 blebs from said strain;

g) a process of creating conserved OMP antigens on the bleb preparation comprising the steps of identifying such antigen, engineering a bacterial strain so as to delete variable regions of a gene encoding said antigen, and making blebs from said strain;

h) a process of reducing expression within the bleb preparation of an antigen which shares a structural similarity with a human structure and may be capable of inducing an auto-immune response in humans, comprising the steps of identifying a gene involved in the biosynthesis of the antigen, engineering a bacterial strain so as to reduce or switch off expression of said gene, and making blebs from  
15 said strain; or

i) a process of upregulating expression of protective OMP antigens within the bleb preparation comprising the steps of identifying such antigen, engineering a bacterial strain so as to introduce into the chromosome one or more further copies of a gene encoding said antigen controlled by a heterologous, stronger  
20 promoter sequence, and making blebs from said strain.

55. A method of immunizing a human host against a disease caused by infection of one or more of the following: *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Haemophilus influenza*, *Moraxella catarrhalis*, *Pseudomonas aeruginosa*, *Chlamydia trachomatis*, *Chlamydia pneumonia*, which method comprises administering to the  
30 host an immunoprotective dose of the bleb preparation of claims 1-34.

56. Use of the bleb preparation of claims 1-34 in the manufacture of a medicament for immunizing a human host against a disease caused by infection of one or more of the following: *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Haemophilus influenza*, *Moraxella catarrhalis*, *Pseudomonas aeruginosa*, *Chlamydia trachomatis*, *Chlamydia pneumonia*.

Figure 1

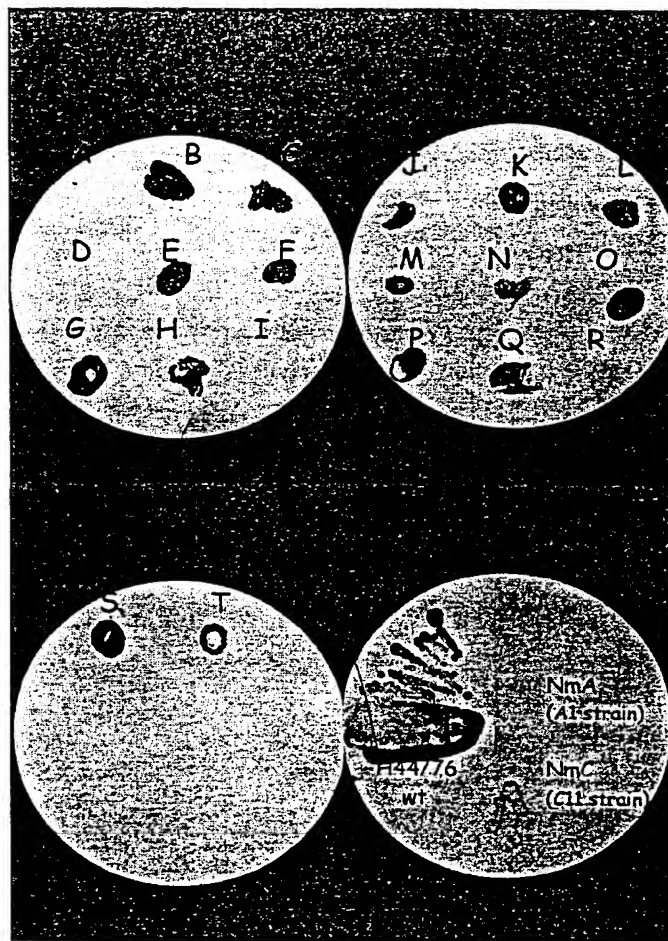


Figure 2

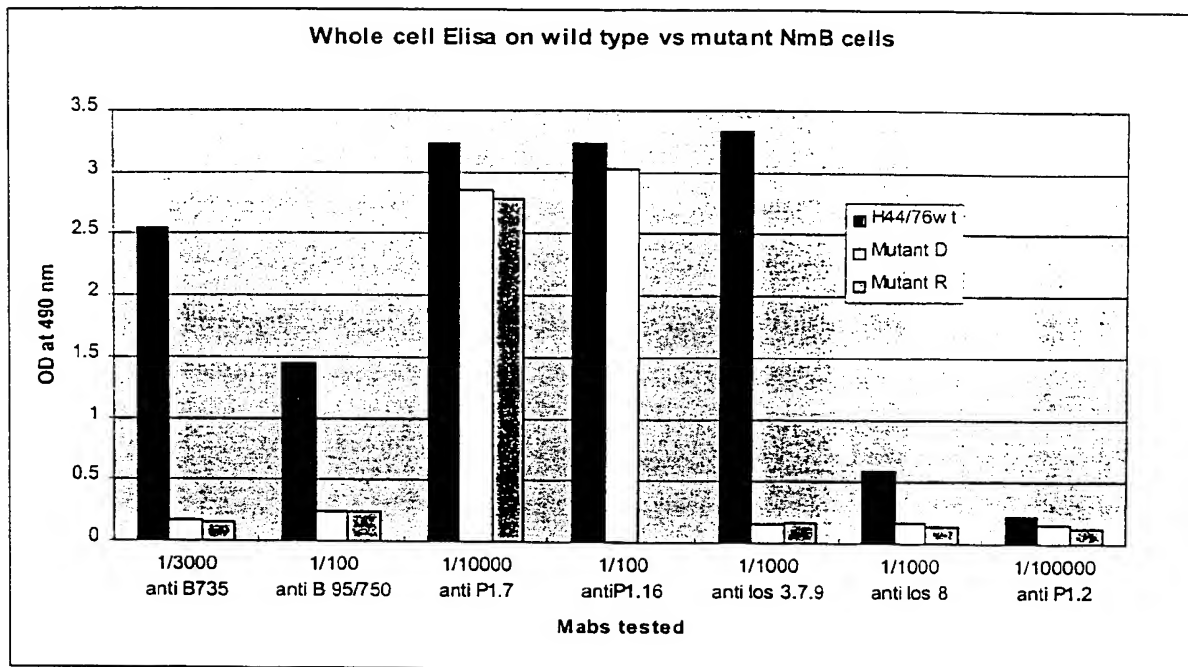


Figure 3

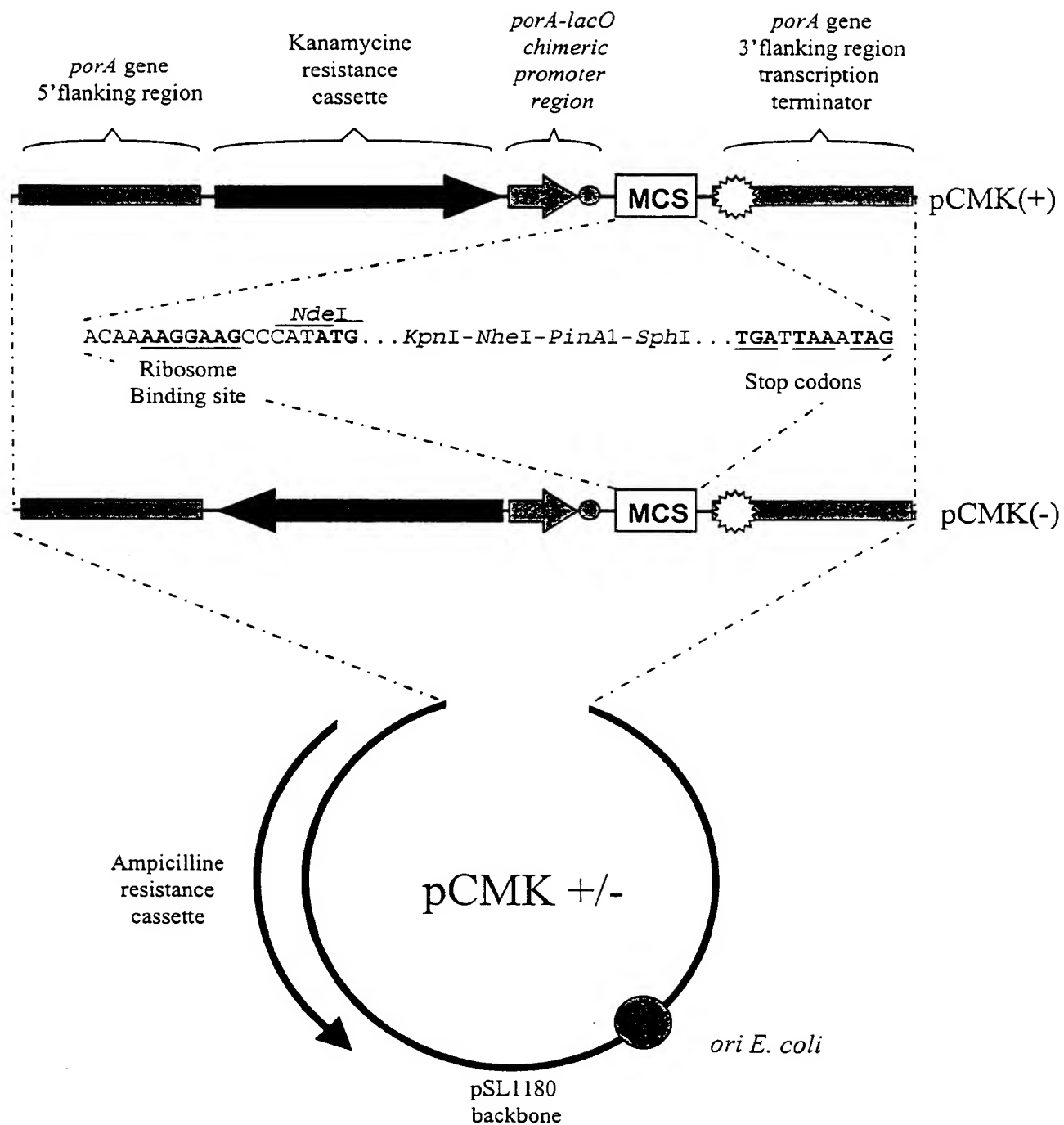


Figure 4

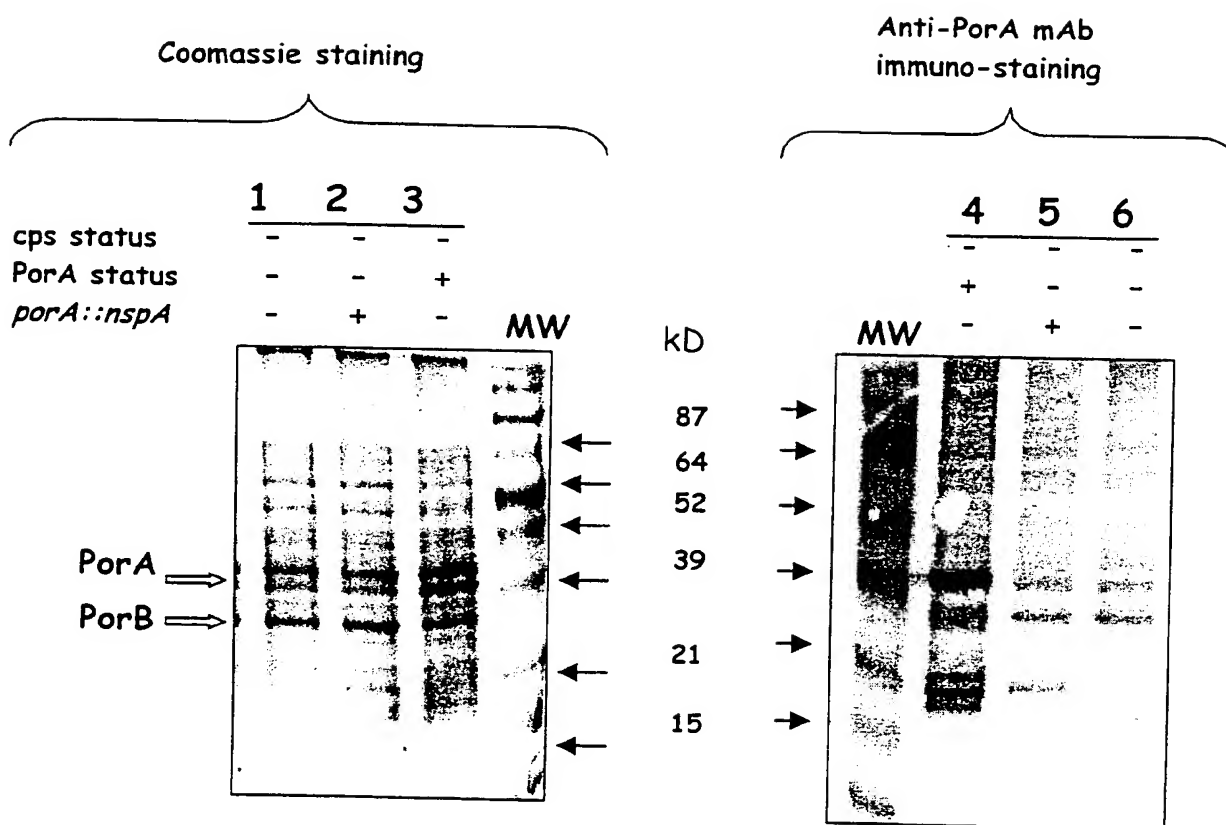


Figure 5

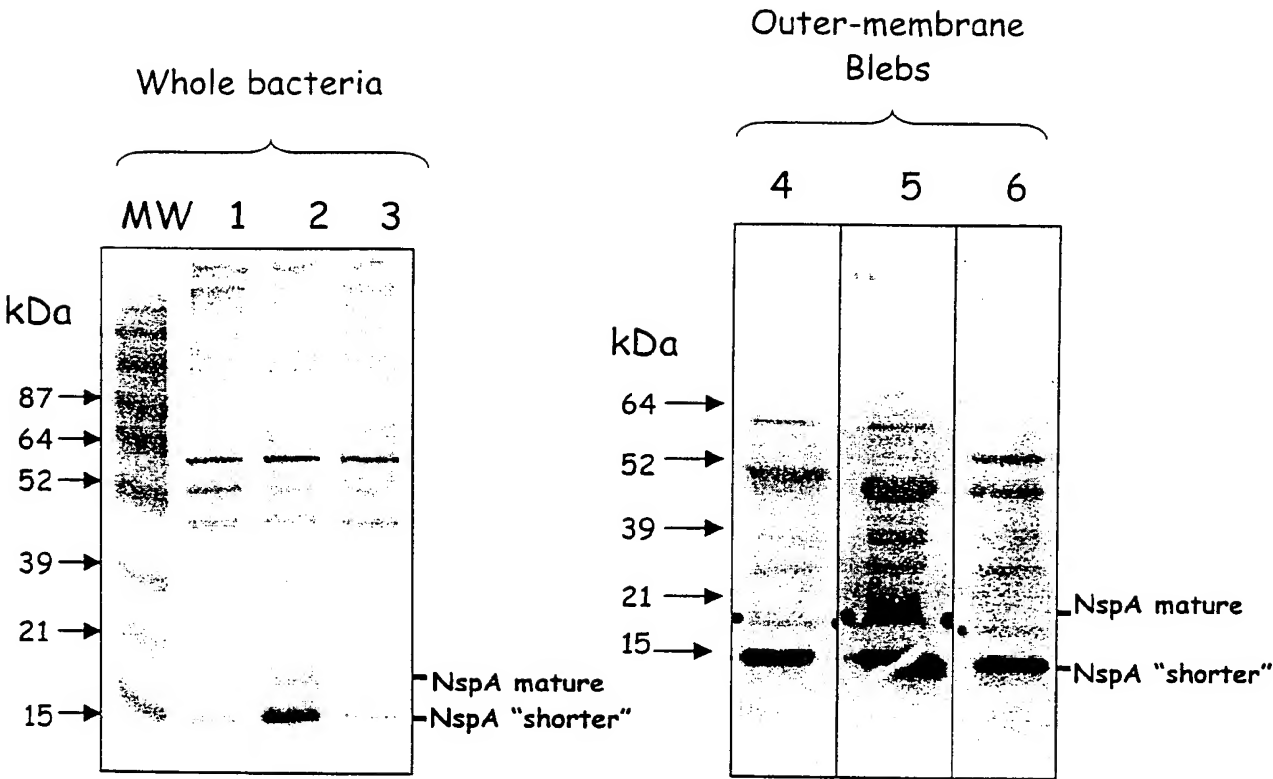




Figure 6

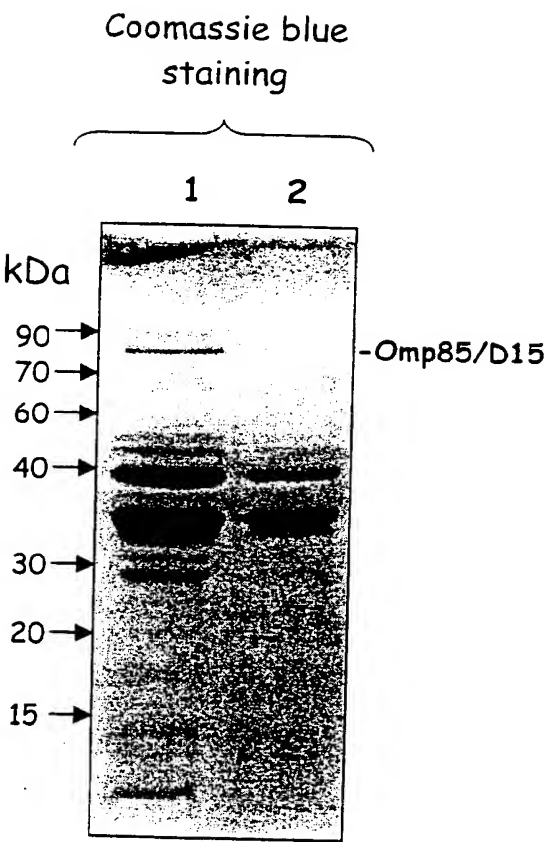


Figure 7

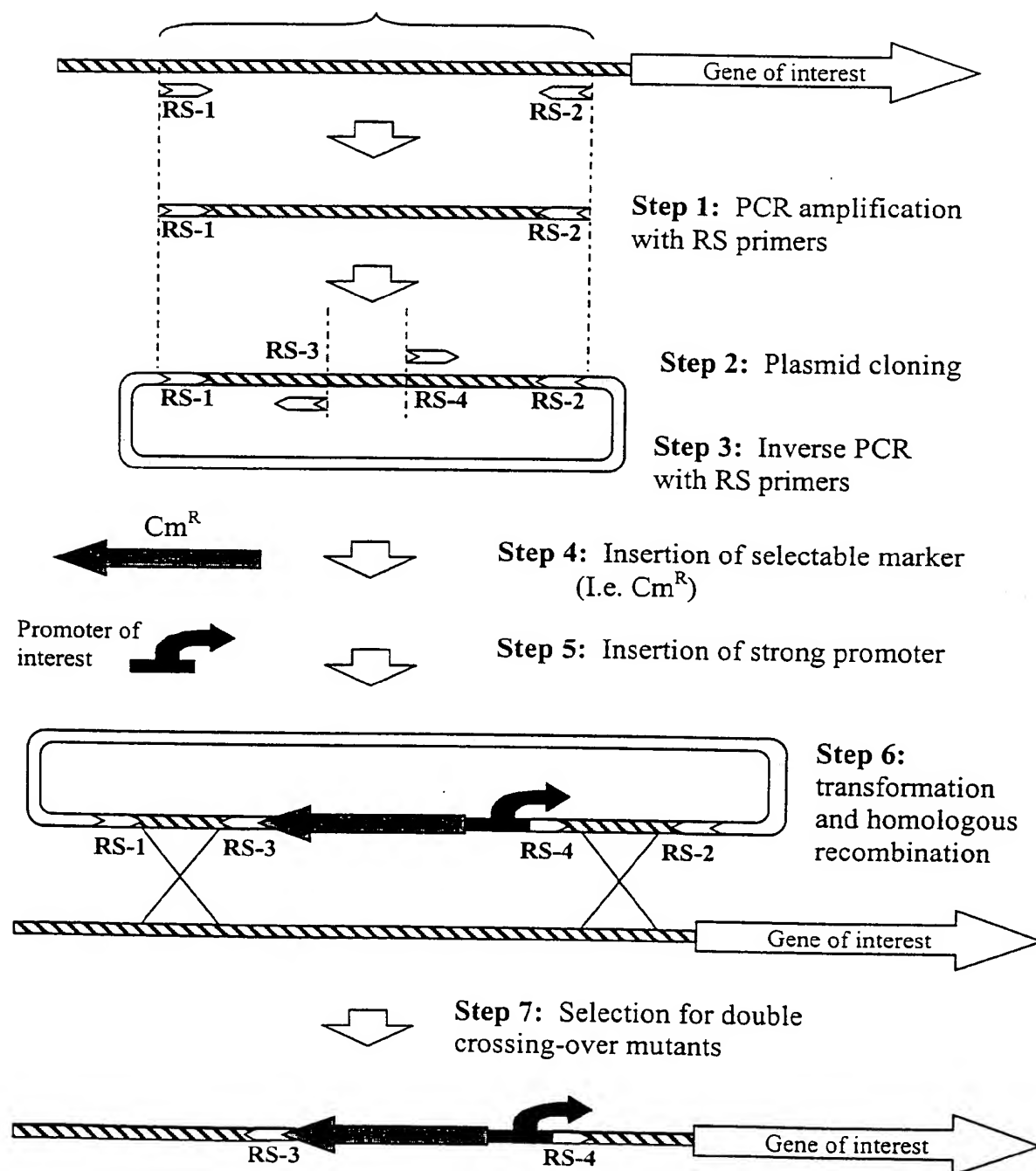


Figure 8

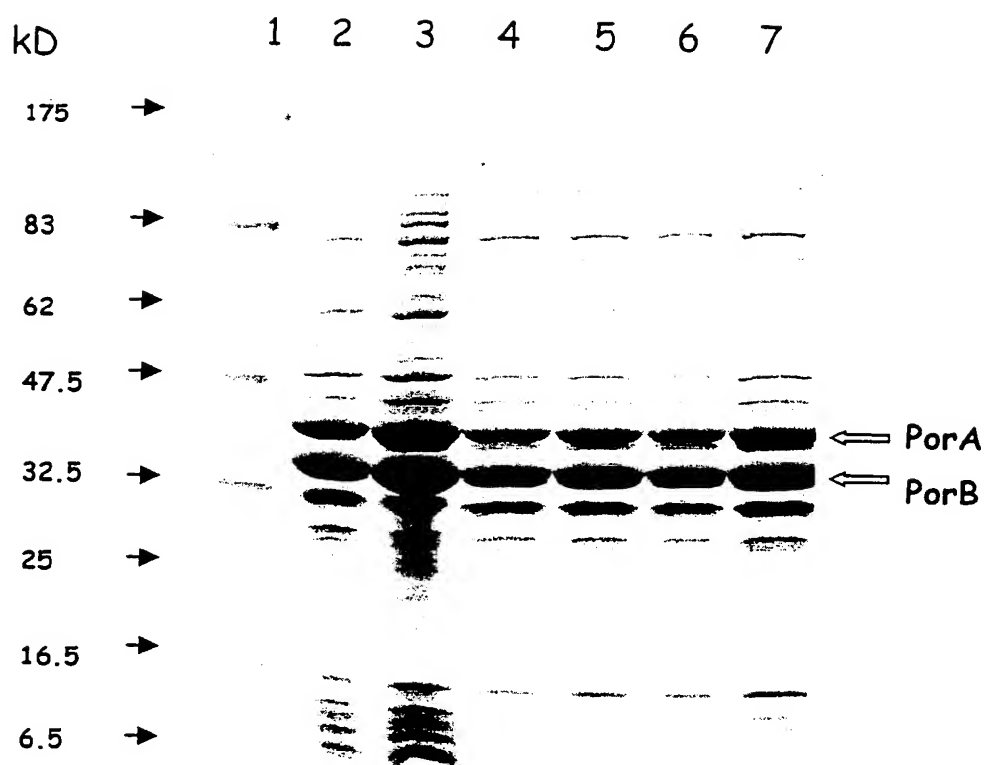


Figure 9

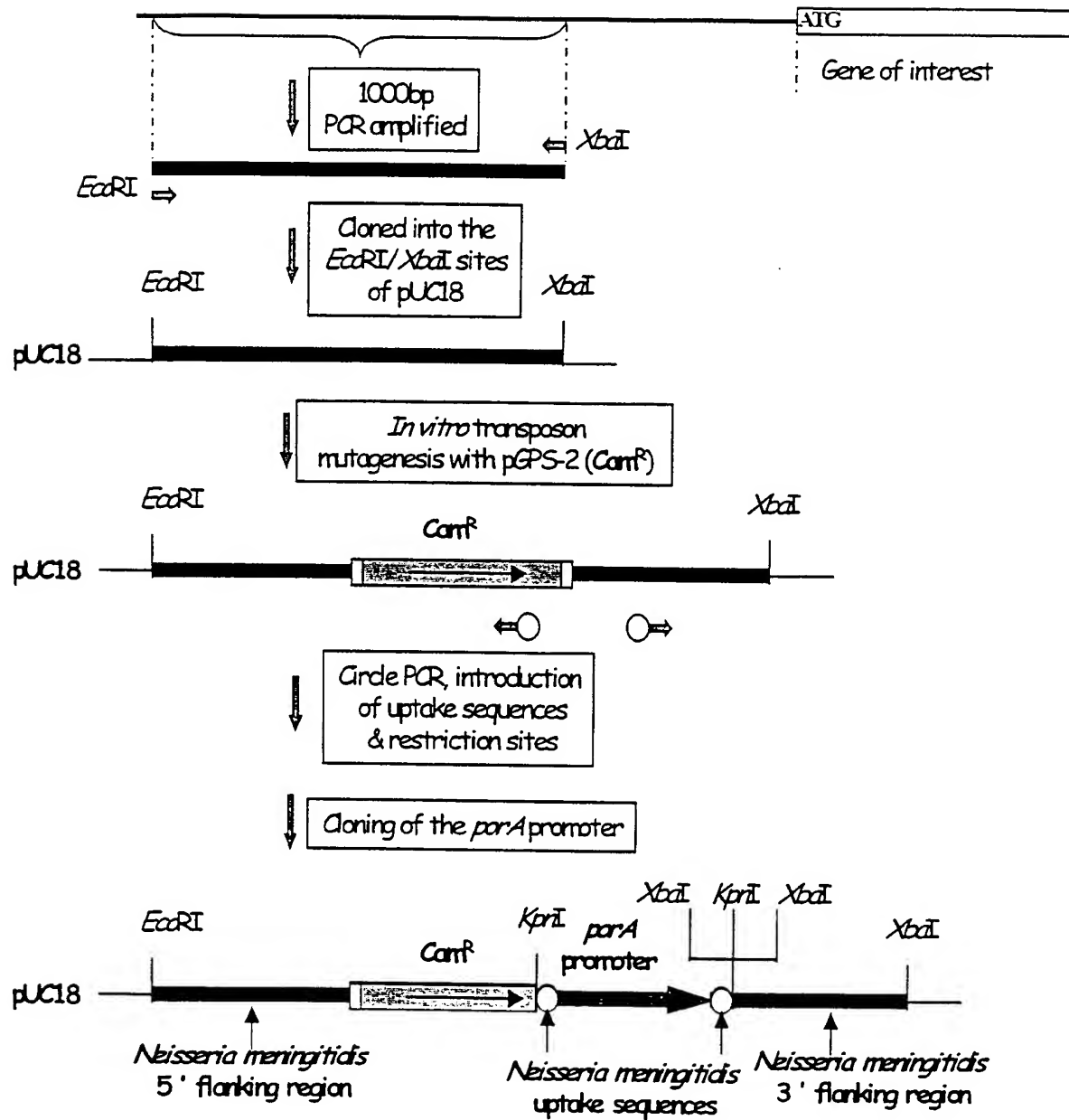
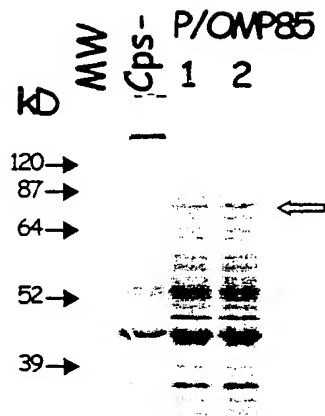


Figure 10

A



B

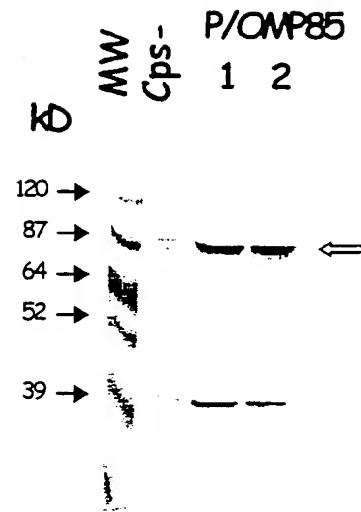
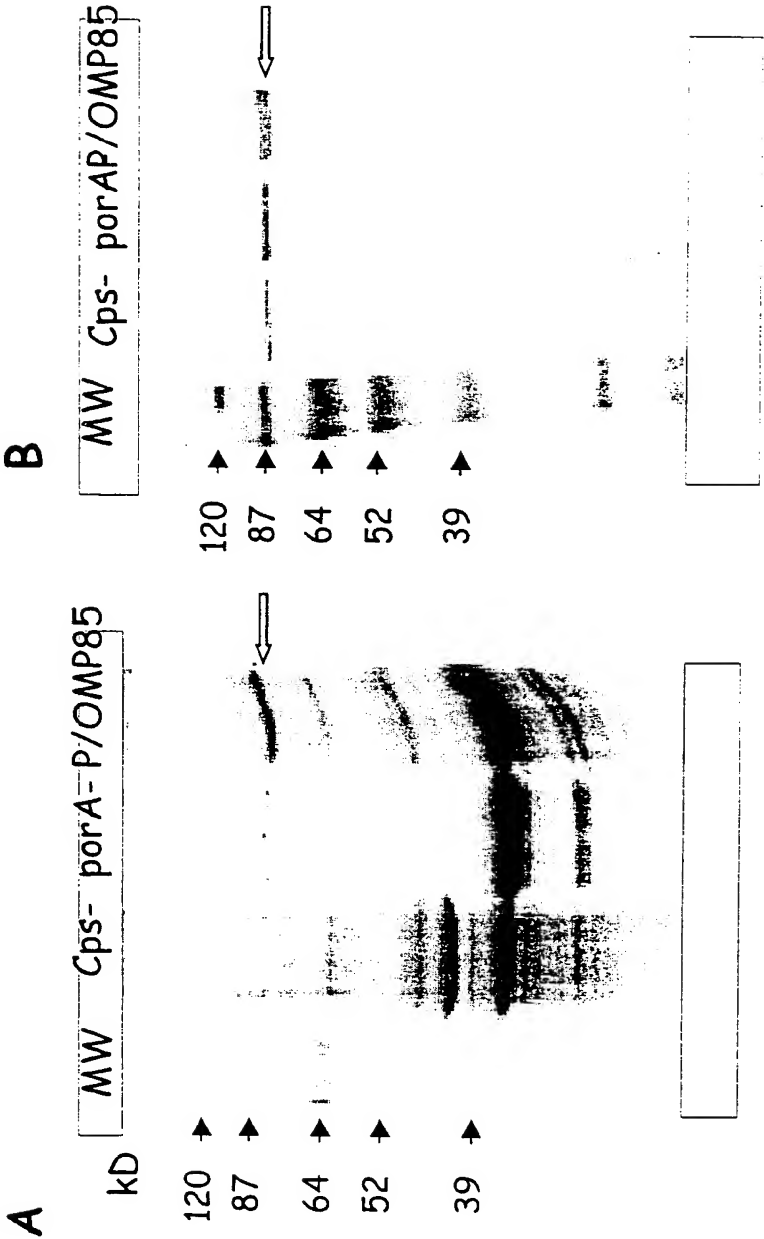


Figure 11



**Figure 12**

Schematic representation of the recombinant PCR strategy used to delete the *lacO* in the chimeric *porA/lacO* promoter.

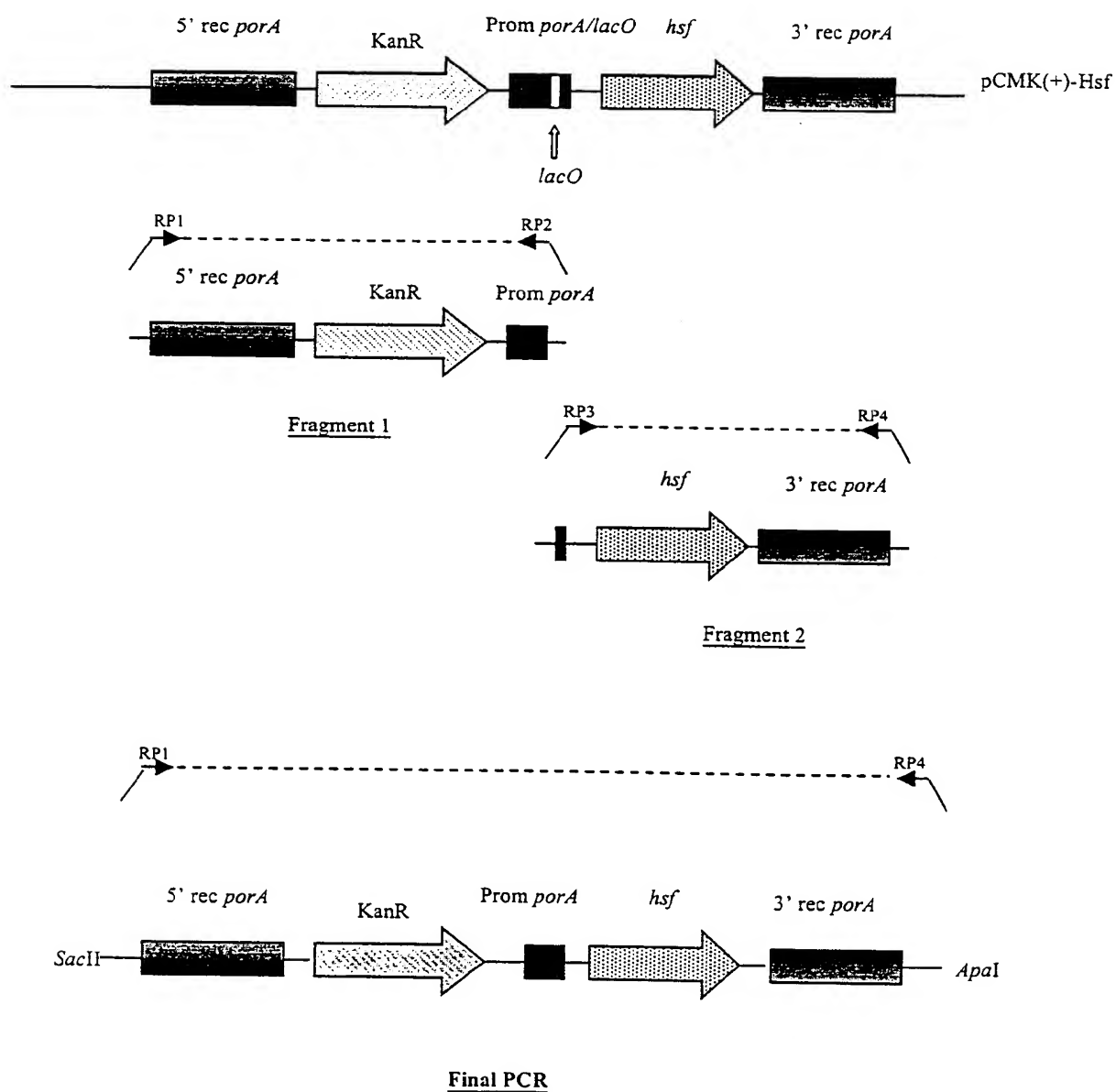


Figure 13

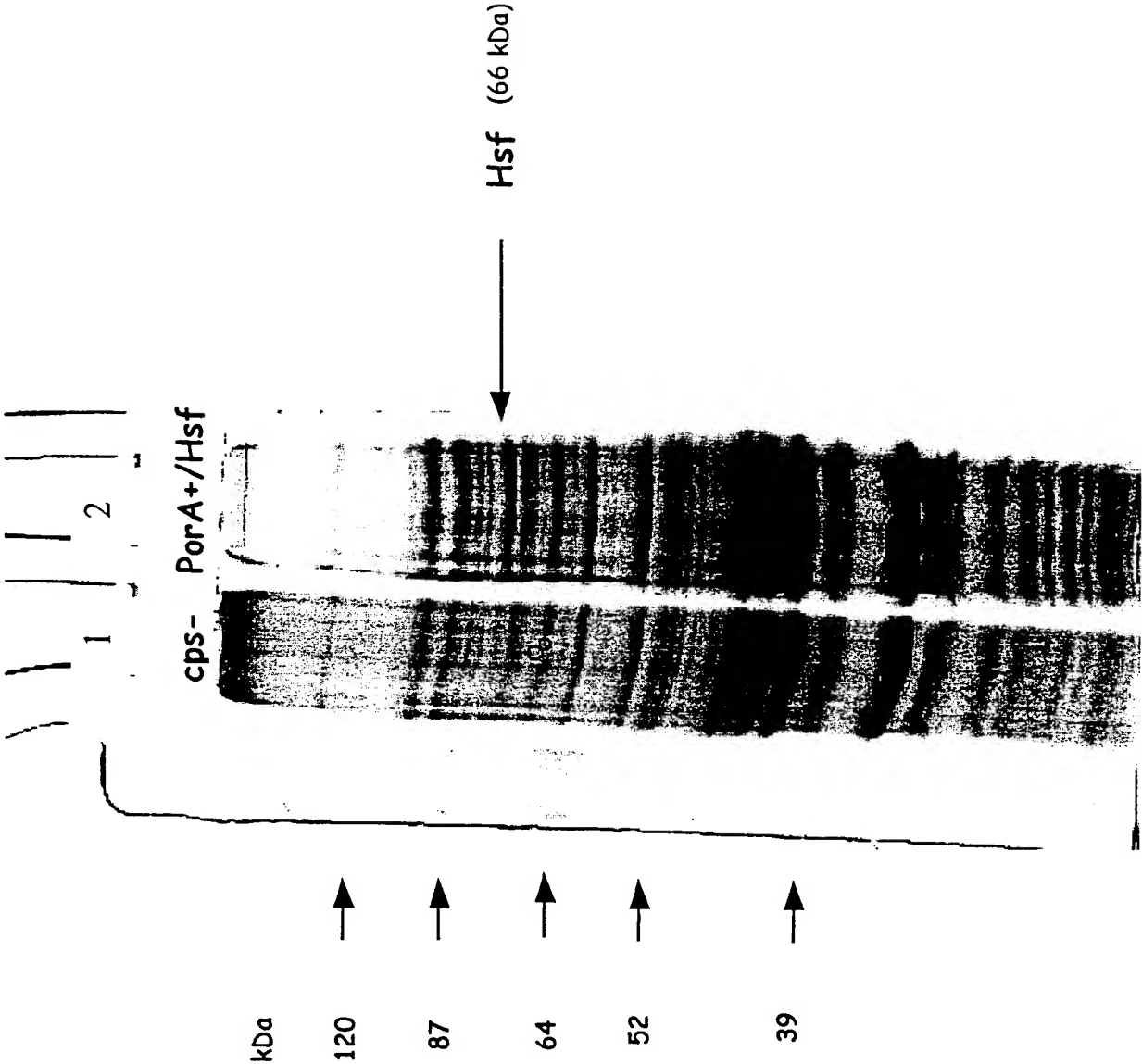
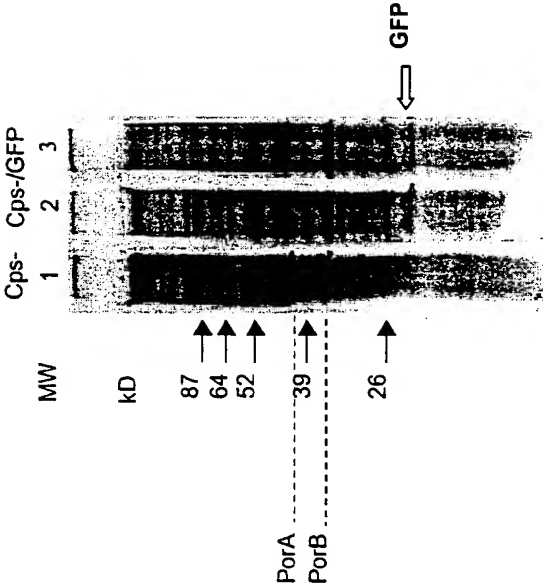




Figure 14



**Figure 15**

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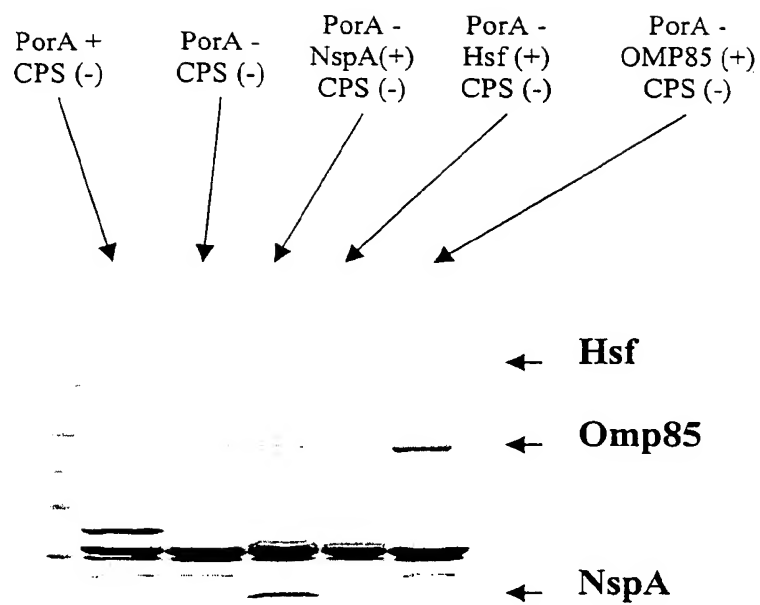


Figure 16

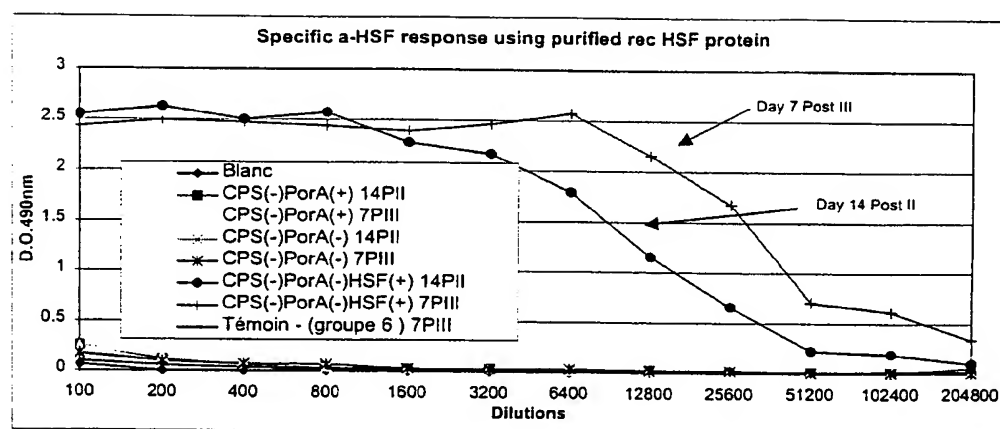


Figure 17

